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OM protein - protein search, using sw model

Run on:	December 3, 2001, 07:13:51 ; Search time 39.47 Seconds (without alignments)
	470.363 Million cell updates/sec

Query Match 23.6%; Score 1032; DB 4; Length 763;  
 Best Local Similarity 33.6%; Pred. No. 8e-76;  
 Matches 285; Conservative 101; Mismatches 249; Indels 212; Gaps 32;

QY	22 SYQLGKHHMGSATKD-NQIAYIDDSKGKAKPNTNKTMQISAEQIVVKITDOG 80   : :  -   :   : :    :     -     :     :     :
RESULT 1	US-08-961-083-66
	; Sequence 66, Application US/08961083
	; Patent No. 6159469
	GENERAL INFORMATION:
	APPLICANT: Choi et. al.
	TITLE OF INVENTION: <i>Streptococcus pneumoniae Antigens and Vaccines</i>
	NUMBER OF SEQUENCES: 452
	CORRESPONDENCE ADDRESS:
	ADDRESSEE: Human Genome Sciences, Inc.
	STREET: 9410 Key West Avenue
	CITY: Rockville
	STATE: Maryland
	COUNTRY: USA
	ZIP: 20850
	COMPUTER READABLE FORM:
	MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
	COMPUTER: HP Vectra 486/33
	OPERATING SYSTEM: MSDOS version 6.2
	SOFTWARE: ASCII Text
	CURRENT APPLICATION DATA:
	APPLICATION NUMBER: US/08/961, 083
	FILING DATE:
	CLASSIFICATION: 435
	PRIOR APPLICATION DATA:
	APPLICATION NUMBER:
	FILING DATE:
	ATTORNEY/AGENT INFORMATION:
	NAME: Brookes, A. Anders
	REGISTRATION NUMBER: 36, 373
	REFERENCE/DOCKET NUMBER: PB340P2
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: (301) 309-8504
	TELEFAX: (301) 309-8512
	INFORMATION FOR SEQ ID NO: 66:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 763 amino acids
	TYPE: amino acid
	STRANDEDNESS: single
	TOPOLOGY: linear
	MOLECULE TYPE: protein
	US-08-961-083-66

ALIGNMENTS

28	121	2.8	2466	3	US-09-080-855-12	Sequence 12, Appli
29	121	2.8	2466	5	PCT-US94-09943-2	Sequence 2, Appli
30	120.5	2.8	542	1	US-08-701-380-2	Sequence 2, Appli
31	120.5	2.8	542	3	US-09-032-365A-13	Sequence 13, Appli
32	120.5	2.8	747	1	US-07-854-596B-40	Sequence 40, Appli
33	120.5	2.8	1181	2	US-08-488-940-2	Sequence 2, Appli
34	120	2.7	2485	4	US-09-290-640-46	Sequence 46, Appli
35	117.5	2.7	672	3	US-09-040-843-4	Sequence 4, Appli
36	117.5	2.7	866	3	US-09-040-843-2	Sequence 2, Appli
37	117	2.7	682	3	US-08-613-009A-10	Sequence 10, Appli
38	117	2.7	702	3	US-08-613-009A-9	Sequence 9, Appli
39	115	2.6	1194	2	US-08-488-940-17	Sequence 1, Appli
40	115	2.6	1194	2	US-08-488-940-18	Sequence 17, Appli
41	115	2.6	1194	2	US-08-296-791-4	Sequence 18, Appli
42	114.5	2.6	1545	4	PCT-US95-10661A-4	Sequence 4, Appli
43	114.5	2.6	1545	5	US-08-867-941-25	Sequence 25, Appli
44	113	2.6	702	2	US-09-074-658-25	Sequence 25, Appli
45	113	2.6	702	4	US-09-074-658-25	Sequence 25, Appli

Db 2 SYELGRHQAGQVKKESNRVSYIDGDQAGQKA--ENLTPDESKREGINAEOXVIKITDQG 59  
 QY ||||| |||:||||:|||||:|||||:|||||:|||||:|||||:|||:|||:|||:|||:|||:  
 Db 60 YVTSHGDHYHYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDDGYVIVKVNNGYYVL 140  
 QY 141 KPGSKRKNIRTQQIAEQAVAKGTKEAKEKGGLAQAHLSEEVAVNEAKRQGRYTTDDGY 200  
 Db 120 KDAAHADNIRTKEEIKRO---KOERSHN---HNSRAD-NAVAARAQGRYTTDDGY 168  
 QY 201 IFSPTDIIDLGDAYLVPHGNHYHYIPKKDLSPSELAAQAWSOKGRGARPSDYRPT 260  
 Db 169 IFNASDIEDTGDAYIVPHGDHYHYIPKNELSASELAEEAWNGKQ--GSRPSSSSYN 226  
 QY 261 APAPGRRKAPIPDVTNPNGQGHQPDNGGYHPAPPRNDAQNKHQRDEFKGKTFKELLQ 320  
 Db 227 A-----NPAQPRLSENHNLTVTP-----TYHON---OGENISSLLRE 260  
 QY 321 LHRLLDKYRHEEDGLIFEPTQVIKSNAFGYVVPHDGHYHILPRSQLSPLLEMELAD--- 376  
 Db 261 LYAKPLSERHVESDLGLIFDPAQITSRTARGVAVPHGNHYHFTPYEQMSELEKRARIPI 320  
 QY 377 RYLAGQTEDDDSGSDHSKPSDKEVTHFLGHRIKAVGKGGLDGKPYDTSDAYVFSKESIHS 436  
 Db 321 RYRSNHWVPD--SRPEQPSPOSTPEPPSPSPQPAFPNPQAPSNSPIDER---LVKEAVRK 373  
 QY 437 VDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAQGQADELAALDQEQQKEKPLFDT 496  
 Db 374 V-----GDGY-----VFEEENGVSRYIPAKDLSAETAAGIDSKLAKQESL--S 413  
 QY 497 KKVSRKVTKDGVGMMPKDGDYFYARDQOLDLTOIAFAEQLMLKDKKKHYRDIVDTGI 556  
 Db 414 HKLGAKKT-----LPSSDREFY--NKAYDL--LARIHQDLDLNKGROVDFEALDNLL 462  
 QY 557 EPRЛАВДВСЛРМНГАГНАТДГССФVIPHIDHTHVVРРYSWLT RDQIATIKYVMQHPEVR 616  
 Db 463 E-RLK-DVXS-----DKVKLV-----XDLAFLAPIRHPE-- 490  
 QY 617 PDIWSKPGEHESSGVIPNVTPLDKRAGMPNWQIHSAAEVQOKALAEGRFATPDGYIFDPR 676  
 Db 491 -----RLGPKNAQITYTDDEIQVAKLAGKYTEDGYIFDPR 526  
 QY 677 DVLAKETFWKDGFSIIPRADGSSLRTINKSLSQAEWQQAQELLAKKNAGDATTDKPK 736  
 Db 527 DITSDE----GDAYVTPHMTHS--HWIKKDSLSEAERAQAYAKEKGL----TPP 572  
 QY 737 EKQQADKSNNQQSEASKEEKESSDDF-IDSLP----- 769  
 Db 573 STDHQDSGNTEAKGAEATYRNVKAKKVPLDRMPYLNQYTVEVKNGSLIIPHYDHYNTR 632  
 QY 770 ----DYGLDRA---TLEDHINOLAQKANIDPKYLIFQP-----EGVQFYN 807  
 Db 633 FEWFDDEGLYEAPKGYTLEDLIATV-----KYYVEHPNERPHSDNGFGNASDHVQ-RN 683  
 QY 808 KNGELVT 814  
 Db 684 KNGOADT 690  
 RESULT 2  
 US-08-961-083-56  
 Sequence 56, Application US/08961083  
 Patent No. 6159469  
 GENERAL INFORMATION:  
 APPLICANT: Choi et. al.  
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
 NUMBER OF SEQUENCES: 452  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA

ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961, 083  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36, 373  
 REFERENCE/DOCKET NUMBER: PB340P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 796 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-961-083-56

Query Match 21.7%; Score 949; DB 4; Length 796;  
 Best Local Similarity 29.5%; Pred. No. 5.1e-69;  
 Matches 277; Conservative 100; Mismatches 214; Indels 348; Gaps 34;  
 Query Match 22 SYOLGKHHMGSATKDNQIAVYDDSKGKAKAPKT-NKTMQDQISAEEGISAQIVWKITDQG 80  
 Db 1 SYELGLYQARTVKENNRVSYID---GKQATQTKTENLTPDEVSKREGINAEOQIVKIKITDQG 57  
 QY 81 YVTSHGDHYHYNGKVPYDAIISELLMTDPNYRFKQSDVINEILDDGYVIVKVNNGYYVL 140  
 Db 58 YVTSHGDHYHYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDDGYVIVKVNNGYYVL 117  
 QY 141 KPGSKRKNIRTQQIAEQAVAKGTKEAKEKGGLAQAHLSEEVAVNEAKRQGRYTTDDGY 200  
 Db 118 KDAAHADNIRTKEEINRQKOEHSOH-REGG-----TPRNDGAVALARSQGRYTTDDGY 169  
 QY 201 IFSPTDIIDLGDAYLVPHGNHYHYIPKKDLSPSELAAQAWSOKGRG--ARPSDYRPT 258  
 Db 170 IFNASDIEDTGDAYIVPHGDHYHYIPKNELSASELAEEAFLS--GRGNLNSRTYR 226  
 QY 259 TAPAPGRRKAPIPDVTNPNGQGHQPDNGGYHPAPPRNDAQNKHQRDEFKGKTFKELL 318  
 Db 227 QNSDNTSRTNW-VPSVS-NPGTTNTNTSN-----NSNTNSQASQNSD----IDSLL 271  
 QY 319 DQLHRLDKYRHEEDGLIFEPTQVIKSNAFGYVVPHDGHYHILPRSQLSPLLEMELAD-- 376  
 Db 272 KQLYKLPLSORHVESDLGLVFDPAQITSRTARGVAVPHGDHYHIFPYSQMSELEERIARII 331  
 QY 377 -RYLAGQTED-----DSGSD----- 391  
 Db 332 PLRYRSNHWVPSRPEQPSQOPTPEPPSPGPQPAFNKLIDSNSLVSQLVRKVGEQYFEE 391  
 QY 392 -----HSKPSDKE-VTHFLGHR-----IKAY----- 412  
 Db 392 KGISRYVFAKDLPSETWKLNLESKISKQESVSHTLTAKKENVAPRDOEFYDKAYNLTTEAH 451  
 QY 413 -----GKGLD-----GKP----- 420  
 Db 452 KALFXNKGGRNSDFQALDKLLELRNDESTNKEKLWDDLLAFLAPITHPERLGKPNQSIETY 511  
 QY 421 -----YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVAN 468  
 Db 512 EDEVRIAQLADKYTTSDGYIFDEHDITISDEGDAYVTPHMGHSHWIGKDSLSDKEVVAQA 571

RESULT 3  
US-08-961-083-182  
; Sequence 182, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452

STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961, 083

FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36, 373  
REFERENCE/DOCKET NUMBER: PB340P2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 182:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

; US-08-961-083-182

Query Match 19.2%; Score 839; DB 4; Length 447;  
 Best Local Similarity 39.9%; Pred. No. 2e-60;  
 Matches 178; Conservative 65; Mismatches 119; Indels 84; Gaps 10

Page 4

QY	36 DNQIAYIDDSKGKAKA P-----TNTKMD-QISAAE-GISA EQIVWV KITDQGYVTSHGDHY	Score 143.5; DB 2; Length 1861; Best Local Similarity 18.3%; Pred. NO. 0.011; Matches 190; Conservative 166; Mismatches 328; Indels 353; Gaps 56;
Db	199 DNK---IPDNQQNANVDKEALNQNKKLDYSVSFDKNGLKNQTVGVNTIE-----	244
QY	90 HFYNGKVPYDAI ISEELLMTDPNYRFKQSDVINEI LDGYVIKV-----GNYYVYL--KP	142
Db	245 ---PQDEVLSGR--VAKPEL LYKETSIETEIA YGEOQI QENPDLAEGT VVRVQEQGP	295
QY	143 GSKRKKNIR-----TKQQIAEQVAKGTKEAKEK GL-----AQVA	175
Db	296 GRKIEVVRIFTVDNAEV SREV LSTKIEATPKIVEKG TKEAKEK GL-----AQVA	355
QY	176 HLSK-----EEVA AVNEAKRQGRYT-TDDGYIFSPTD IDDLG-----DAYLVP	218
Db	356 PLPEYTG VQSGA IVEPEQV ASLPE-----YSGTL SG A IVEPEQV EPIGGVQSGA IVEPEQV	409
QY	219 HGNHYHYIPKKD-----LSPSELAAQAYWSQSQGRGAR PSDYR RTP-----A	261
Db	410 E---QVTPLPEYTG TQAGAVV SPEQV APLPEYTG TQSGA IVEPAQV TPLPEYTG VQSGA	465
QY	262 PAPRRKAPIPD-----VTPNP-----GQ	280
Db	466 IVKPAQV TPLPEYTG TQSGA IVEPEQV APLPEYTG VQSGA	525
QY	281 GHQPD-----NGGYH PAPP RPN D-----ASQ NKH QRD E-FKGKTF KELLD-QLHRL-D	325
Db	526 IVEPEQV EPQ EYTG TQSGA IVEPEQV AEP AENP TEKA QEP KEQOK QEP EK NIEL RNV SDV ELYSLAD	585
QY	326 LK YR-H VEDGL-----IFEP-TQ VIKSNAFGYV VPHGDHYH IPR S	365
Db	586 GK YKQH VS LDA IAPSNO ENYFVKV KSSKF KD VFL PI SIVD STK DGQP V-----YK ITASA	640
QY	366 QLSPLEMELADRYLAG QTED DSGSDHSKPSKD KEVTH-TFLGH RIKAYKG KGLDG KPYD TS	424
Db	641 E--KLKQDVNNKY-----EDNF TFLAKKAER EVNFTSF SNLVQAINN NLNGTYLA A	692
QY	425 DAYFSKESIHSV DKSGV TAKHGDHF HYIG FGELEQ YELDEV ANWV KAK-----GQADE	478
Db	693 -----SLNANE VELENG-----ASSYIKGRFTG KLF GSKD G	723
QY	479 LAALDOE QGKE KPL FDT KKVS-----RK VT KDGK --VG YMM PKDG KDFY ARD QDL	529
Db	724 KNYAI---YNLKKPLFDTLSAATV ENLT LKD VNIS GKT DIGA L-----ANE ANNA	770
QY	530 TQI AFAEQ EML KDKK-----HYR YD IV D-----TG	555
Db	771 TRIN NVH VD GVL AGER GIGGL VNKAD NSK ISNS SFK GRIV NSV ET KAP YNIG GLV QQL TG	830
QY	556 I-----EP RL A DVSS LPM HAGN ATY DTG-----SSF V I PHID HI H-----	591
Db	831 IN ALV DK SKAT ITI SS-----NAD STN QTV GGL VLAG LVEK DALIS NSY AEGN INN V KRG SV A	887
QY	592 -VV PYSW LTRD QIATI KYVMQH PEV RPD IWSK PGHE EGS V I PNL D K RAG MPN--WQ	648
Db	888 GVAG YLW-DR DS-SE ERHAG RL HNV L S D I N VMNG NAI SGYHY RGMR ITD SY SNK DNR VYK	945
QY	649 I-IHSAEEVQKALAEGRFATPDGYIFDPRDV LAKETF VV WKDG SF SI PRAD GSSL RTINK S	707
Db	946 VTE LEK DEV VTKES LEER-----GTILD VD SQI ASK KSEI--NSL SAP KV ET LL STN KES	997
QY	708 DL SQA E WQ Q A Q ELLA KKA-----G DAT DTD K--PKE KQ QAD KS NEN QO	749
Db	998 DF SKV KDV Q A S R A LAY KNT EKL LPF Y NKAT I V KG NL V KED ST LYE KEI L S A V MM K D NEV	1057
QY	750 PSE ASK E EKES DDF IDSL LPD YGL DR--AT LED HIN QLA QKA NI DP KYL IFO PEG VQF YN	807
Db	1058 ITDIASHKE-AANKL LIH KDH S SEK L D LITY Q SDF SKL AE-YRV GDT GLI YTP N-QFL Q	1113
QY	808 KN GEL VTY DIK TLQ OIN	824
Db	1114 NH SIV NEV L PDL KAV D	1130
RESULT 5 PCT-US93-07261-11		
Sequence 11, Application PC/TUS9307261		
GENERAL INFORMATION:		
TITLE OF INVENTION: PFEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF		
NUMBER OF SEQUENCES: 23		
CORRESPONDENCE ADDRESS: ADDRESSEE: John H. C. Blasdale		
STREET: One Gir alda Farms		
CITY: Madison		
STATE: New Jersey		
COUNTRY: USA		
ZIP: 07940-1000		
COMPUTER READABLE FORM:		
MEDIUM TYPE: FLOPPY disk		
COMPUTER: Apple Macintosh		
OPERATING SYSTEM: Macintosh 6.0.5		
SOFTWARE: Microsoft Word 5.1a		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: PCT/US93/07261		
FILING DATE: 19930805		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 07/927,531		
FILING DATE: 07-AUG-1992		
ATTORNEY/AGENT INFORMATION:		
NAME: Blasdale, John H. C.		
REGISTRATION NUMBER: 31,895		
REFERENCE/DOCKET NUMBER: DX0288K		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 201-822-7398		
TELEFAX: 201-822-7039		
INFORMATION FOR SEQ ID NO: 11:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 158 amino acids		
TYPE: amino acid		
TOPOLogy: linear		
MOLECULE TYPE: protein		
PCT-US93-07261-11		
Query Match 3.3%; Score 142.5; DB 5; Length 1588; Best Local Similarity 20.0%; Pred. No. 0.01; Matches 174; Conservative 120; Mismatches 341; Indels 233; Gaps 38;		
QY	27 KHHMG SAT KDN QIAYIDDSKGKAKA PKT N-----KTM DQI SAEE GISA EQIVWV KITDQGY	81
Db	4 KEALK QKTEKNEKAR NALKE KKE KKLKE QKND A QKAD LTK KES QD S S E K S L K E E K N K I K D N N D E A L K N K G N D K D D	106
QY	82 V TSH GDH YHF YNGKVPYD A I ISEELLMTDP NYRF KQSDV IN ELDG--YV IKV NGN-----G LA QVA	175
Db	64 KEKE-----N KET L K K E L E N Q K E E K N K I K D N N D E A L K N K G N D K D D	166
QY	136 -YV V YL KPG SKR K N I R-----TK QQIAEQV AKG TKEAKEK-----G LA QVA	175
Db	107 K KIVPKK PES V E K D L K E M E L K E F I K OHL K D Y E E R K R R N W I L R S L R D K L R E T E Q L E	945
QY	176 H L SKEE V A V N E A K-----R O G R Y T D D G Y I F S P T D-----I D D L	211
Db	167 K L N A Q L E S A I N E L K E R R A S R R P M M V K M Q R G M K D E W E D E W I K K Y D Q E A K N G T K D E E I K D K	226
QY	212 G D A Y -L V P -H G M H Y H I P K K D L S P S E L A A Q A Y W S Q O R G R A P S D Y R P T P A P A P G R	266



QY 735 PKEKQQADKSNENOOPSEASKEEKESD 762  
Db 750 AKGKEVTNKAHEN-----LEEYNETD 770

RESULT 7  
US-08-596-291-3  
; Sequence 3, Application US/08596291  
; Patent No. 5821075

GENERAL INFORMATION:  
; APPLICANT: GONEZ, LEONEL JORGE  
; APPLICANT: SARAS, JAN  
; APPLICANT: CLAESSEN-WELSH, LENA  
; APPLICANT: HELDIN, CARL-HENRIK  
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/596, 291  
; FILING DATE: 09-AUG-1996  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/115, 573  
; FILING DATE: 01-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GATES, EDWARD R.  
; REGISTRATION NUMBER: 31, 616  
; REFERENCE/DOCKET NUMBER: LO461/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEFAX: 617/720-2441  
; TELEX: 92-1742 EZEKIEL  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2465 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-596-291-3

RESULT 8  
US-09-100-804-3  
; Sequence 3, Application US/09100804  
; Patent No. 6066472

GENERAL INFORMATION:  
; APPLICANT: GONEZ, LEONEL JORGE  
; APPLICANT: SARAS, JAN  
; APPLICANT: CLAESSEN-WELSH, LENA  
; APPLICANT: HELDIN, CARL-HENRIK  
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:

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QY 204 PTDLDDLGDAYL-----VPHGNHYH1PKKDLSPSELAAQAYWSOKQGRGARPSDY 256  
Db 1647 PANISNSTWSSALHQTLSNMVSQAQSHEAPK---SQEDTICTMFYVPOKIPNKPEFEDS 1703

QY 257 RPTPAPAPGRRKAPIPDVTNPQGQHOPDNGGYHPAPPNDAONKHORDEFKGKTFKE 316  
Db 1704 NPSPLP-----PDMA--PGOSYQPOS----ESASSSSMDKYHIIHISEPTROE 1745

QY 317 LLDQLHRLDKYRVEEDGLIFE-PTOVIKSN-AFGYVWPHGDHYHILPRSQLSLEM 373  
Db 1746 NWTPPL-KNDLE-NHLEDFELEVLLITLIKSEKASLGFITVTKGN-----Q 1788

QY 374 LADRYLLAGQTEDDSDGSDHSKPSDK-----EVTHFLGHRIKAYKG---LDGK 419  
Db 1789 RIGCYVHDVIQDPAKSDGRLKPGDRLIKVNNTDVNTNMTHDAVNLLRAASKTVRLVIGRV 1848

QY 420 PVDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWKAKGOADEL 479  
Db 1849 PRITQNTNVASFATGH-----KLTNCNEEL 1873

QY 480 AAALDQEQQKEKPLFDTKVKSRKVTDGKVGVYMMPKDQDLYFQYARDQDLTQIAFAEQEL 539  
Db 1874 GFSL--CGGHDSDLQVWVYIS-----DINPRSAATECNL 1905

QY 540 MLKDKKKHYRDIVDTG-----EPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHIVVPS 596  
Db 1906 QLLDVTHYVNGVSTQGMTEEVNRALDM-SLPSLVLKATR-----NDLPVVPS 1953

QY 597 WLTRDQIATKVMQHPEVRPDIWSKPGHEESGSVI-PNVTPLDKRAGMPNQWQIHSAAE 655  
Db 1954 --KRSAVSA-----PKSTKGNGSYSVGSCSQPALTPNDSFSTV-----AGEE 1993

QY 656 VQK-ALAEGRFATPDGYIF--DPRDVLAKEFTVWKDGFSIIPRADGSSLRTINKSDLSQLA 712  
Db 1994 INEISYPKGKCST--YQIKGSPNLTLPKESYIQEDDIY----DDSQEAEVIQSLLDVV 2045

QY 713 EWQQAQELLAKKN-AGDA-----TDTD--KPKEKQQADKSN---- 745  
Db 2046 D-EEAQNLLNNENNAAGDSCCGPGTLKMNGKLSEERTEDDCDGSPLEFYTEAKMNGCEE 2104

QY 746 --ENQQPSEA--SKEEEKESDD----FIDSLPDYGLDRATED 780  
Db 2105 YCEEKVKSESLIQQPQEKKTDDDEITWGNDLPL---IERTNHED 2145

APPLICATION NUMBER: US/09/100,804  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/596,291  
 FILING DATE: 09-AUG-1996  
 APPLICATION NUMBER: US 08/115,573  
 FILING DATE: 01-SEP-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/09943  
 FILING DATE: 01-SEP-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GATES, EDWARD R.  
 REGISTRATION NUMBER: 31,616  
 REFERENCE/DOCKET NUMBER: LO461/7003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-720-3500  
 TELEX: 617-720-2441  
 INVESTIGATOR INFORMATION:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2465 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-100-804-3

RESULT 9  
 US-08-296-791-3  
 Sequence 3, Application US/08296791  
 Patent No. 6245337

## GENERAL INFORMATION:

APPLICANT: St. Geme III, Joseph W.

ATTORNEY: Falkow, Stanley

TITLE OF INVENTION: Haemophilus Adherence and Penetration

NUMBER OF INVENTION: Protein

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296,791

FILING DATE: 25-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INVESTIGATOR INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 1541 amino acids

TYPE: amino acid

TOPOLOGY: unknown

US-08-296-791-3

Query Match

Best Local Similarity 3.0%; Score 131.5; DB 4; Length 1541;

Matches 153; Conservative 111; Mismatches 294; Indels 315; Gaps 37;

Db 1906 QLLDVIHYWNGVSTQGMILEEVNRAIDM-SLPSLVLKATR-----: : ||| |

Qy 597 WLTRDQIATIKYVMQHPEVRDIWISKPGHEESGVI-PNVTPLDKRAGMPNWQIHSAAE 655

Db 1954 -KRSAVSA-----PKSTKGNGSYSVGSCSQPALTPNDSFSTV-----AGEE 1993

Qy 656 VQK-ALAEGRFATPDGYIF--DPRDVLAKETFWKDGFSFIPRADGSSLRTINKSDLSQA 712

Db 1994 INEISYPKGKCST---YQIKGSPNLTLPKESYIQEDDIY----DDSQEAEVIQSLILDVV 2045

Qy 713 EWQQAQELLAKKN-AGDA-----TDTD--KPKEKQOADSNS--- 745

Db 2046 D-EEAQNLLNNENNAAGDSCCGPGTLKMNGKLSEERTEDTDCDGSPLEPYFTEATKMGCEE 2104

Qy 746 --ENQOPSEA--SKEEEKESDD---FIDSLPDYGLDRATLED 780

Db 2105 YCEEKVKSESLIQLPKQEKKTDDDEITWGNDELP--IERTNHED 2145

Query Match

Best Local Similarity 19.9%; Score 133; DB 3; Length 2465;

Matches 176; Conservative 114; Mismatches 322; Indels 272; Gaps 44;

Qy 9 GSVAAILLATHIGSYQLGKHM---GSATKDNOIAYTIDDSSKGAKAPKTNTKMD-QISAE 64

Db 1422 GQVWHILKEK--GQSPTSKEHVPVTPQCTLSDQNA---QGQGPEKVKKTTQWKDYSFVTE 1476

Qy 65 EGISAEQIVVKITDQGYVTSHGDHYHFYNKGVPYDATIISEELLMTDPNVRFRKFQSDVINEI 124

Db 1477 ENTFEVKLFLKNSSGLGFSFRED--NLIPEQINASIVRVKKLFGAQPAAESGKIDVGDV 1534

Qy 125 LDGYVIKVNGNYVYVLKPGSKRKKNIRT-----KQQ 154

Db 1535 L-----KVNG---ASLKGQLSQQEVLARLTAREPVELLCRPPGVLPEDTALLTPLQS 1586

Qy 155 TAEQVAKGTKEAKEKGGLAQWAHLSSKEEVAVNEAK----RQRRTT---DDGYIFS 203

Db 1587 PAQVLPNSSKDSSQSPSCVEQSTSSDENEMSDSKKKQCKSPRRDSDSYSGGSGEDDLVTA 1646

Qy 204 PTDIIDDLGDAYL-----VPHGNHYHYIPKKDLSPSELAAQAYWSQKQGRGARPSDY 256

Db 1647 PANISNSTWSSALHQTLSNMVSQAOSHHEAPK---SQEDTICTMFYYPQKIPNKPEFEDS 1703

Qy 257 RPTPAPAPGRRKAPIDVTPNPGQGHOPDNGGYHYPAPPNDASONQKHQRDEFKGKTFKE 316

Db 1704 NPSPLP-----PDMA--PGQSYQPQS-----ESASSSSMDKYHIHHISEPTROE 1745

Qy 317 LLDQLHLRDLKRYRVEEDGLIFE-PTQVQSN--AFGYVYVPHGDHYHILIPRSQLPLEME 373

Db 1746 NWTPPL-KNDLE-NHIEDFELEVELLITLIKSEKASLIGFTVTKGN-----Q 1788

Qy 374 LADRYLAGOTEDDDSGSDHSKPSDK-----EVTHFLGRRIKAYGKG---LDGK 419

Db 1789 RIGCYVHDVIQDPAKSDGRLKPGDRLIKVNNTDVTNMTDAVNLLRAASKTVRLVIGRV 1848

Query Match

Best Local Similarity 17.5%; Score 131.5; DB 4; Length 1541;

Matches 153; Conservative 111; Mismatches 294; Indels 315; Gaps 37;

Db 1849 PRITQNTNVASFATGH-----KLTNCNEEL 1873

Qy 420 PYDTSDAYVFSKESTHSVDSKGGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADEL 479

Db 444 DSKGKAKA-----PKTNKTMQDQISAEQIVVKITDQGYVTSHGDHYHFYNKG 95

Db 462 DNKGSLKVGDGTWILKQQTNGSGQHAFASVGIVSGRSTLVLNDDKQVDPNSIYFCFRGR 521

Qy 96 -----VPYDAI-----ISBELLMTDPN--YRFKQSDVIN- 122

Db 522 LDNGNSLTEDDHIRNIDDGARLVLVNHMTNASNITITGESLITDPTNIDAPDEDNP 581

QY 123 ----EILDG---YVIKVNGNYVVLKPGSKRKNI-----RTKQQIAEQVA 160  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 582 YAFRRIKDGQQLYLNLNEYTYALRKASTRSELPKNSGESNENWLYMGKTSDEAKRNVM 641  
 QY 161 K-----GTKEAKEKGGLAQVAHLSKEEVAAVNEAKRQGRYTDDGYIFSPTD 206  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 642 NHINNERMNGFNGYFGEEEGKNNGNLNTFKGSE-----QNRFLLTGG----TN 687  
 QY 207 IIDDL---GDAYL---VPHGNHYHYI--PKKD--LSPSELAAQAWSQKQGRGARPS 254  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 688 LNGDLTVEKGTLFLSGRPTPHARDIAGISSTKKDPHFAENNEVVVEDDWNR 739  
 QY 255 DYRPTPAPGRRKAPIPDVTNPQGQHOPDNGGYHPAPPNPDASQNKHQ----- 305  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 784 TVCVRSDYTGVCTTDKLSKALN-----SFNPTNLRGNVNLTESANFVLG 830  
 QY 345 KSNAGFVVVPHGD-----HYHIIIPRSQSLPLEMELADRYLAGOTEDDDSGSDHSKP 395  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 740 -----NFKATTMNVT----GNASLYSGRNVANITSNITASNKAQVHIGYKTGD 783  
 QY 306 ---RDEFKGK---TFKELLDQLHLRDLKYRVEEDGLIFEPTQVI----- 344  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 784 TVCVRSDYTGVCTTDKLSKALN-----SFNPTNLRGNVNLTESANFVLG 830  
 QY 396 SDKEVTHFLGHRRIKAYGKGLDGKPYDTSDAYVFSKESIHSDVKSGVTAKHGDHFHYIGF 455  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 877 AD-----NSNNVTKYNTLTVNLSLNG-----SFYVL-- 903  
 QY 456 GELEYQELDEVANWVAKGQAD-ELAALDLQEQGKEKPLFDTKVSRKVTKDGKVGYMMMP 514  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 904 TDLSNKQGDKVWVTKSATGNFTLQVADKTGEPHNHNLTLFDASKAQRDHNLNVSLVG-- 959  
 QY 515 KDGKDYFYARDQDLTQIAFAEOLMLKDKKHRYDIVDTGIEPR-----L 560  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 960 -----NTVDLGAWKYKLRLN-----NGRYDLYNPEVEKRNQTVDTTNITTPNNI 1003  
 QY 561 AVDVSSLPMHAGNATYDTGSSFYIPHIDHIVWVPSWLTRDQIATIKVVMQHPEVRPDIW 620  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1004 QADVPSVP-----SNNEEIARVDEAPVPPAPAT-----PSETTEV 1040  
 QY 621 SKPGHEESGSVIPNVTPLDKRAGMPNQWQLIHSAAEVOKALAEGRFATPDGYIFDPRDVL 680  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1041 AENSQEKSTKEVNEQDATETAQ-NREVAKEAKSNVKANTOTNEVAQSG--SETKETOT 1097  
 QY 681 KETFWWDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELLAKKNAGDATDTKPKEQ- 739  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1098 TET-----KETATEVEKEEAKVETEKTOEV----PKVTSQVSPKQEQS 1136  
 QY 740 -----QADKSNENQOPSEASKEEKESESDDFIDS 767  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1137 ETVQPQAREPAREN-DPTVNIKEPQSQTNTTADT 1168

RESULT 10  
 PCT-US95-10661A-3  
 Sequence 3, Application PC/TUS9510661A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Washington University, et al.  
 ; TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/10661A  
 FILING DATE: 16-AUG-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/296,791  
 FILING DATE: 25-AUG-1994  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Trecartin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: FP-59941/RFT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1541 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 PCT-US95-10661A-3

Query Match 3.0%; Score 131.5; DB 5; Length 1541;  
 Best Local Similarity 17.5%; Pred. No. 0.078;  
 Matches 153; Conservative 111; Mismatches 294; Indels 315; Gaps 37;

Query Match 3.0%; Score 131.5; DB 5; Length 1541;  
 Best Local Similarity 17.5%; Pred. No. 0.078;  
 Matches 153; Conservative 111; Mismatches 294; Indels 315; Gaps 37;

QY 44 DSKGAKA-----PKTNTKTMQDQISAEEGISAEQIVWKITDQGYVTSHGDHYHYNGK 95  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 462 DNKGSLKVQDGTVILKQQTNGSGQHAFASVGVSRSTLVNLDDQVDPNSIYFFGRGGR 521  
 QY 96 -----VPYDAI-----ISEELLMTDPN---YRFKQSDVIN- 122  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 522 LDINGNSLTFDHIRNIDDGARLNVHNMTNASNITITGESLITDPNTITPYNIDAPDEDNP 581  
 QY 123 ----EILDG---YVIKVNGNYVVLKPGSKRKNI-----RTKQQIAEQVA 160  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 582 YAFRRIKDGQQLYLNLNEYTYALRKASTRSELPKNSGESNENWLYMGKTSDEAKRNVM 641  
 QY 642 NHINNERMNGFNGYFGEEEGKNNGNLNTFKGSE-----QNRFLLTGG----TN 687  
 QY 207 IIDDL---GDAYL---VPHGNHYHYI--PKKD--LSPSELAAQAWSQKQGRGARPS 254  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 688 LNGDLTVEKGTLFLSGRPTPHARDIAGISSTKKDPHFAENNEVVVEDDWNR 739  
 QY 345 KSNAGFVVVPHGD-----HYHIIIPRSQSLPLEMELADRYLAGOTEDDDSGSDHSKP 395.  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 831 KANLFGTIQSRGNSQVRLTENSHWHLTGNSDVHQLLA-----NGHIHLNS 876  
 QY 396 SDKEVTHFLGHRRIKAYGKGLDGKPYDTSDAYVFSKESIHSDVKSGVTAKHGDHFHYIGF 455  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 877 AD-----NSNNVTKYNTLTVNLSLNG-----SFYVL-- 903  
 QY 456 GELEYQELDEVANWVAKGQAD-ELAALDLQEQGKEKPLFDTKVSRKVTKDGKVGYMMMP 514  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 904 TDLSNKQGDKVWVTKSATGNFTLQVADKTGEPHNHNLTLFDASKAQRDHNLNVSLVG-- 959  
 QY 515 KDGKDYFYARDQDLTQIAFAEOLMLKDKKHRYDIVDTGIEPR-----L 560  
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 960 -----NTVDLGAWKYKLRLN-----NGRYDLYNPEVEKRNQTVDTTNITTPNNI 1003  
 QY 561 AVDVSSLPMHAGNATYDTGSSFYIPHIDHIVWVPSWLTRDQIATIKVVMQHPEVRPDIW 620

Query Match 2.9%; Score 128.5; DB 2; Length 1076;  
 Best Local Similarity 20.1%; Pred. No. 0.08;  
 Matches 141; Conservative 87; Mismatches 244; Indels 231; Gaps 40;

QY 621 SKPGHEESGSVIPNVTPLDKRAGMPNWQIHTSAEEVQKALAEGRFATPDGYIFDPRDVLA 680  
 Db 1041 AENSKQESKTVEKNEQDATETTAQ-NREVAKEAKSNVKANTQTNEVAQSG- SETKETQT 1097

QY 681 KETFWKDGSFSIPRADGSSLRTINKSDLSQAEWQQAELLAKKNAGDATDDKPKEQ- 739  
 Db 1098 TET-----KETATEVEKEEAKVETKTQEV----PKVTSQVSPKQEQS 1136

QY 740 ----QADKSNEQQPSEASKEEKEESDFIDS 767  
 Db 1137 ETVQPOAEPAREN-DPTVNIKEPQSQTNTTADT 1168

RESULT 11  
 US-08-867-941-19  
 ; Sequence 19, Application US/08867941  
 ; Patent No. 5977337  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M  
 ; APPLICANT: Du, Run-Pan  
 ; APPLICANT: Wang, Quijun  
 ; APPLICANT: Yang, Yan-Ping  
 ; APPLICANT: Klein, Michel H  
 TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
 NUMBER OF SEQUENCES: 67  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: 6th Floor, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/867, 941  
 FILING DATE: 03-JUN-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24, 973  
 REFERENCE/DOCKET NUMBER: 1038-681 MISS:jb  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1076 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-867-941-19

RESULT 12  
 US-09-074-658-19  
 ; Sequence 19, Application US/09074658  
 ; Patent No. 6184371  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M  
 ; APPLICANT: Run-Pan Du  
 ; APPLICANT: Quijun Wang  
 ; APPLICANT: Yang, Yan-Ping  
 ; APPLICANT: Klein, Michel H  
 TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
 NUMBER OF SEQUENCES: 78  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: 6th Floor, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/074, 658  
 FILING DATE: 08-MAY-1998  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24, 973  
 REFERENCE/DOCKET NUMBER: 1038-795  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1076 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-074-658-19

---

Query Match 2.9%; Score 128.5; DB 4; Length 1076;  
 Best Local Similarity 20.1%; Pred. No. 0.08;  
 Matches 141; Conservative 87; Mismatches 244; Indels 231; Gaps 40;

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QY 3 KTYGYIGSVAILLATHIGSYOLGK---HHMGSATKDNOIAYI---DD--SKGK--- 48
Db 148 KNYAAGGAINEIEY-ENRVSVEISKGANSEYYSGALSGSVAFTVKTADDI IKDGKDWWGV 206
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QY 49 ---AKAPKTNKTMDOQISAEGISAEQIVWKITD---QGYVTSHGDHYHFYNGKVVPYDAI 101
Db 207 QTKTAVASKNNAWVNSVAAGKAGSFSGLLIYTDRRGQEY-KAHDD---AYQGSQSFDRA 262

QY 102 ISEELLMTDPNYRFKOSDVINEILDGYVIVKVNNGNYYVYLKPG---SKRNIRTQOIA 156
Db 263 VA---T'DDPNNR--TELIANECD----ANGNYEACAAGGQTQLQAKPTNVRDKVNVK 309

QY 157 EQVAKG-----TKEAKEKGLAQV AHLS-KEEVAAVNEAKRQGRYTTDDGYIFSPTDII 208
Db 310 DYTGPNRLIPNPPLTQDSKSLLRPGYQLNNDKHVYGGVETIKQ-NYAMQDKTV----- 361

QY 209 DLLGDAYLVPHGNHYHYIPKKDLSPSEL---AAAQAYWSQOKQGRGARPSDYRPTPAPAG 265
Db 362 ---PAYLAVH-----DIEKRSLSNHAQANGYY-OGNNLGERIRD----- 396

QY 266 RRKAPITPDVTNPQGQHOPDNGGYHPAPPNPDASQNKHQRDEF-----KGKTFK 315
Db 397 -----TIGPDSGYGINYAHGVFY-----DEKHQKDRLGLEYVVDSKGENKWFID 439

QY 316 ELLDQHLRSDL-----KRYHVEEDGL--IFEPTQVIKSNAFGYVVPH----- 355
Db 440 DVRSVSYDKQDITLRSQINTHCSTYPHIDKNCTPDVNKPF SVKEVDNNAYKEQHNLIKAV 499

QY 356 -----GDHYHILPR-----SQLSPLEMELADRYLAGT EDDSGSDHSKPSDKEV 400
Db 500 FNKKMALGSTHHHINLQVGYDKFNSSLRSRVEYRLA-----THQSYQKLQDYTPPSNP-- 550

QY 401 THTFLGHRIKAYKGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQ 460
Db 551 ----LPDKFKPI-LGSNNKPKI-CLDAYGYGH-----HPQACNAKNSTYQNFIAKKGIEQ 599

QY 461 YELDEVANWVAKGOADEL--AAALDQ--EQGKEKPLFDTKVKSR-----KVTKGKVGY 511
Db 600 Y-----NQKTNTDKIDYQAITDQYDKQNPNSTLKPFEKIKQSLQGQEKYKINKIDEGLF 650

QY 512 MMPKD-----GKDYFYARDQDLTQIAFAEQELMLKDKHHYRIDIV 552
Db 651 KAYKDLRNEWAGWTNDNSQQNANKGTDNQY-----PNQATVVKDDK-CKYS-- 696

QY 553 DTGIEPRLAVDSSLPMHAGNATYDTGSSFVIPHIDIHVVPY 595
Db 697 ----ETNSYADCSTTPRHI-----SGDNYFIALKDNMTINKY 729

RESULT 13  
 US-08-663-112-2  
 Sequence 2, Application US/08663112  
 Patent No. 5849503  
 GENERAL INFORMATION:  
 APPLICANT: WAGATSUMA, Masako  
 APPLICANT: KURITA, No. 58495031ko  
 TITLE OF INVENTION: MUTANT PROTEINS OF HUMAN DNA  
 TITLE OF INVENTION: TOPOISOMERASE I

---

NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ADDRESSEE: Dunner L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/663,112  
 FILING DATE: 26-NOV-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Einaudi, Carolyn P.  
 REGISTRATION NUMBER: 32,220  
 REFERENCE/DOCKET NUMBER: 06609.1488-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 765 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-663-112-2

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Query Match 2.9%; Score 127; DB 2; Length 765;  
 Best Local Similarity 20.1%; Pred. No. 0.063;  
 Matches 137; Conservative 90; Mismatches 240; Indels 214; Gaps 34;

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QY 141 KPGSKRKNIRTQKQIAEQVAKGTKEAKEKGLAQV AHLSK-----EEVAAVNEAK 189
Db 42 KDREREKSKHNSNSEHKDSEKKHEKEKTKHKDGSSEKHKDKHDKRKEKVRASGDAK 101
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QY 190 RQGRYTTDGYIFSPTDILID-LGDAYLVPHGNHYHYIPKKDLSPSELAAQAYWSOKQG 248
Db 102 I--KKEKEENGF-SSPPQIKEDEPEDDGYFVP-----PKEDIKP-----LKR P 139

QY 249 RGARPSDYRPTPAPAGRKAPIPDV-TPNPGQHOPDNGGYHPAPPNPDASQNKHORD 307
Db 140 RDEDDVYKPKKIKTEDTKKEKKRKL EEEEDGKLKKPKNKKDKKKPKEE 199

QY 308 EFKGKTFKELLDQLHRLDKYRHEEDGLIFEPT-----QVTK----- 345
Db 200 EOKWKWEE--ERYPEGIKWKFILEHKGPVFAAPPYEPPLPENVKFYDGKVMKLSPKAEV 256

QY 346 SNAFGYVVPH-----GDHYHILPRSQLSPLEMELADRYLAGT E 384
Db 257 ATFFAKMLDHEYTTEKIFRKNNFKDWRKEMTNEEKNIT--TNLSKCDFTOMSQYKAOTE 314

QY 385 DDDSGSDHSKPSDKEVTHFLGHRIKAYKGKGLDGKPYDTSDAYVFSKESI--HSVDSKGV 442
Db 315 ARKQMSKEEKLKIKEENEKL---KEYG----FCIMDH--KERIANFKIEPPGL 360

QY 443 TAKHGDHFHYIGFGELEQYELDE--VANWVAKGOADELAALDQEQGKEKPLFDTKVK- 499
Db 361 FRGRGNH---PKMGMLKRRIMPELDIINCSK-----DAKVSPSPPGHKWKVEV 405

QY 500 -SRKV-----KGKVGYMM-----PKDGKDYFYARDQDLTQIAFAEQELML 541
Db 406 HDNKVWTWVSWTENIQSGSIKYMLNPSSRIKGEKDQWVETAR-----RLKKCVD 455

QY 542 KDKKHYRDIVDTGIEPR---LAVDVSSLPMHAGN---ATYDTGS--SFVIPHID-- 588
Db 456 KIRNQYREDWKSKEMKVRQARALYFIDKLALRAGNEKEEGETADTVGCCSLRVEHNLH 515

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QY 589 -----HIVVVPYSWLTRDQIATIKYVMQHPEVRPDIWSKPGHEESGSVIPNVTPLDKRAG 643
Db 516 PELDGQEIVVFDFLGLKD--SIRYY-----NKVPUERKRV- 547
Db 548 FKNLQLFMEHQ-----PEDDLFDRNLNTGILNKHLDLMEG-----LTAKVF 589
QY 702 RTINKSDLSQAEWQQAOELLA 722
Db 590 RTFNASITLQ---QQLKELTA 607

RESULT 14
5231168-2
; Patent No. 5231168
; APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;
; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.
; TITLE OF INVENTION: MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409,658
; FILING DATE: 18-SEP-1989
; SEQ ID NO:2:
; LENGTH: 783
; 5231168-2

Query Match 2.98; Score 127; DB 6; Length 783;
Best Local Similarity 17.98; Pred. No. 0.065;
Matches 153; Conservative 147; Mismatches 309; Indels 246; Gaps
QY 41 YIDDSKKGKAKAPKTNKTMQDQISAAEG------ISAEQTIVVKITDQGYVTSHGDH 88
Db 2 FVESEKSEHEAEN---EESSELEEGHHEEIVPEQNNEESGESKLVDNDEGGFEAHHEN 57
QY 89 Y--HFYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDGYVIKVNGNNYVYLKPGSKR 146
Db 58 FSSEEVNSSELNENEFVESDKSVTPE--AEHEEVSE-----ESNPEPAENEESI 105
QY 147 KNIRTQQIAEQVAKGTKEAKEKGLAQHLSKEEVAAVNEAKRQGRYTTDDGYIFSPD 206
Db 106 EEAHQEEIVPEQ---NDEESGESGLVD-----NE---EGDFEENHEEFEPDQ 147
QY 207 IIDDLGDAYLVPH-----GNHYHYIPKKDLS-PSE-----LAAAQAYWSOKQG 248
Db 148 NDSELSENELVESEKSVEPAEHVEIVSEKSVSEPAEHVEIVSEKSTSEPAEHVESVSEQ 207
QY 249 RGARPSDYRPTPAPAPGRRKAPTIDVTPN--PGQGHQPDNGGYHPAPPNDAS----300
Db 208 SNNEPSEKKDGPVPSKPFEEIEKVDVQPKIVDLOITEPNFVDSOPNPQEPVPEPSFKIEK 267
QY 301 ----ONKHQRDEFKGKTFKELLDQLHRLDKYRHEEDGLIFEPTQVIKSNAFGYVVPHG 309
Db 268 VPSEEENKHASVDPEVKE-KENVSEV-----VEEKQNSQESVEEIPVNE-----309
QY 357 DHYHTIPRSOLSPLEMELADRYLAGOTEDDDSGSDHSKPS---DKEVTHFLGHRKAYG 413
Db 310 DEFEDVHTEQOLD-----LDHKTVDPPEIVEEVEIIPSELHENEVAH-----348
QY 414 KGLDGKPYDTS DAYVFSK-----ESIHSVVKSGVTAKHGDHFHYIGFGELEQYELDEV 466
Db 349 -----PEIVEIEEVFPEPNQNNEFQEINEEDDKSA-----HI-----QHEIVEV 386
QY 467 ANWKAKQOADELAAALDQEOGKEKPLFDIKVSRKVTKGKVGYMMPKDGKDYFYARDQ 526
Db 387 -----EELPEDDKNEKEVHEIVE-----VEILPEDKNEKEVHEIVE-----LPEDKNE-----I 461
QY 527 LDLTQIAFAEQEMLKDKKHYR--YDIVDTGIEPRVLAVDVSSLPMHAGNATYDTGSSFVI 584
Db 420 HEIVEV-----EELPEDDKNEKEVHEIVE-----LPEDKNE-----I KGQ 461

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Query Match          2.88; Score 124; DB 4; Length 1848;
Best Local Similarity 16.98; Pred. No. 0.42;
Matches 155; Conservative 125; Mismatches 336; Indels 302; Gaps
Qy   48 KAKAPKTNKTMDQISAEQIVVKITDQGYVTSHGDHYHFYNGK-----VPYDA 100
Db   487 KOKADANNKV--QAFSQVGVSGRSTLVLNDDKKQVDPNSIYFGFRGGRLLNGNSLTFDH 544
Qy   101 I-----ISEELLMTDPN---YRFKQSDVINEILDGYVIKV-- 132
Db   511 --NEKVQHEIVEEILPEDIKNEKGQHEIVEV-EELPEDKNEKGQHEIVEV-EEILPEDK-- 510
Db   462 VEVEEI-----LPEDKNEKGQHEIVEV-EELPEDKNEKGQHEIVEV-EEILPEDK 703
Qy   644 MPNWOIHSAAEVQKALAEGRFATPDGYIFDPRDVLAKETFVWKGFSIPRADGSSLRT 703
Db   566 EDKNEVQHEIVEEILPEDIKNEKGQHEIVEV-EELPEDKNEKGQHEIVEV-EEILPEDK 565
Qy   756 EEEKESSDFID--SLPDYGLDRATLEDHINQLAQANIDPKYLIFQPEGVQFYNGELV 813
Db   626 PEEKNEFSVVEKAIPQ-----EPVVPTLNENENVTPK-----PSEGEST 665
Qy   814 TYD--IKTLQQINP 825
Db   666 KPDIVQIKIVQENKP 680

RESULT 15
US-08-296-791-6
; Sequence 6, Application US/08296791
; Patent No. 6245337
; GENERAL INFORMATION:
; APPLICANT: St. Geme III, Joseph W.
; APPLICANT: Falkow, Stanley
; TITLE OF INVENTION: Haemophilus Adherence and Penetration
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,791
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1848 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-08-296-791-6

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Db 545 IRNIDDDGARVNHNMTNTSNTITGESLITNPNTITSYNEAQD-----DDHPLRIRSI 598  
 Qy 133 -----NGNYVYVLKPGSKRKNI-----RTKQQIAEQVAKGTKEAK 167  
 | : | : | : | : | : | : |  
 Db 599 PYRQLYFNQDNRSYTLKKGASTRSELPPQNSGESNEENLYMGRTSDAAKRNVMNHINNER 658  
 Qy 168 EKGLAQVAHLSKEEVAVNEAK-----RQGRYTDDGYIFSPTDIIDDLGDAYLVP 218  
 | : | : | : | : | : | : |  
 Db 659 MNGFN--GYFGEETKATQNGKLNVTFNGKSDQNRELLTGG----TNLNGDLN---- 705  
 Qy 219 HGNHYHYIPKDLSPSELAAAQAWSOKRGARPSDYRPTPAPGRRKAPIPDVTNP 278  
 | : | : | : | : | : | : |  
 Db 706 -----VEKGTLFLSG-----RPTP----- 719  
 Qy 279 GQGHQPDNGGYHPPAPPRNDAQSQN-KHQDEFKGKTFKELLDQLHRLDLKYRHVEEDGLI 337  
 | : | : | : | : | : | : |  
 Db 720 ---HARDIAGISSTKKDPHETENNEVVVEDDWINRNFK----- 754  
 Qy 338 FEPTQVIKSNAFGYVVPHDHYIIIPRSQSLPELEMADRYLAGQT---EDDSG--SDH 392  
 | : | : | : | : | : | : | : | : |  
 Db 755 -ATTMNVTIGNASLY---SGRNVANITSNITASNNAQVHIGKTYGKTDTCVRSVDTGYVUTCH 810  
 Qy 393 SKPSDKEVTHFLGHRIKAYKGKGLDGKPYDTS DAYVFSKESIHHSVDKSGVTAKHGDHFHY 452  
 | : | : | : | : | : | : | : | : |  
 Db 811 NSNLSEKALNSFNPTNLRGNVNLTEASFTLGKANLFG--TIOSIGTSQVNILKENSHWHL 868  
 | : | : | : | : | : | : | : |  
 Qy 453 IGFGELEQYELDEVANWVKAKGOADELAALDQEQQKEKPLFDTKVSRKVTKDGKVGYM 512  
 | : | : | : | : | : | : | : |  
 Db 869 TGNSNVNLNTNGHIHINAQNDANKVT-----YNTLTVN-----S 905  
 | : | : | : | : | : | : |  
 Qy 513 MPKDGDKYFYA----RDQDLTQIAFAEQEQLMLKDK---KHYRYDIVTGIEPRLAV 562  
 | : | : | : | : | : | : | : |  
 Db 906 LSGNGSFYWWDFTNKSNKUVNKSATGNFTLQVADKTGEPNHNELTIFDASNATR-- 962  
 | : | : | : | : | : | : |  
 Qy 563 DVSSLPMHAGNATYDTGSSFVIPHIDHIVVYPWSWLTRDQIATIKYVMQHPEVRPDIWK 622  
 | : | : | : | : | : | : |  
 Db 963 --NNLEVTLANGSVDRG-----AW-----KYKLRNNNGRYDLYN- 994  
 | : | : | : | : | : | : |  
 Qy 623 PGHEEGSVIPN---VTPLDKRAGMPNWQ-----IIHSAAEVOKALAEGRFAT 667  
 | : | : | : | : | : | : |  
 Db 995 PEVEKRNQTVDTTNITTPNDIQADAPSQAQNNEEIAARVETPVPPPAPATESAIASEQPET 1054  
 | : | : | : | : | : | : |  
 Qy 668 PDGYTFDPDVLAKETFWKDGSFSIPRADGSSLRTINKSDLSOAEW----OOAQE 719  
 | : | : | : | : | : | : |  
 Db 1055 RPAETAQP---AMEETNTANSTETAPKSQTATQENPNSSEVPSETTEKVAENPPQENE 1110  
 | : | : | : | : | : | : |  
 Qy 720 LLAKKNA-----GDATDTKP-----KEKQODKSNEOOPSEASEEKEESD 762  
 | : | : | : | : | : | : |  
 Db 1111 TVAKNQEATEPTPONGEVAKEDQPTVEANTQTNEATQSEGKTEETOTAE-TKSEPTESV 1169  
 | : | : | : | : | : | : |  
 Qy 763 DFIDSLPPDYGLDRATLEDHINOLAQKANID-----PKYLIFQPEGVQFFYN 807  
 | : | : | : | : | : | : |  
 Db 1170 TVSENQPEKTVSQSTEDKVVEKEEKAKVETEETOKAPQVTSKEPPKQAEPAPEEV-TD 1228  
 | : | : | : | : | : | : |  
 Qy 808 KNGELVTVYDIKTLOQINP 825  
 | : | : | : | : | : | : |  
 Db 1229 TNAE---EAQALQQTQ 1242

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 3, 2001, 07:16:03 ; Search time 39.47 seconds  
(without alignments)  
451.548 Million cell updates/sec

Title: US-09-645-835A-4  
Perfect score: 4080  
Sequence: 1 MTKKVVILVGLLSQLTL.....DHDHEHENEAKDEQNHAD 792

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Issued\_Patents\_AA:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	322.5	7.9	746	5	PCT-US95-10509-2
2	233	5.7	447	4	US-08-961-083-182
3	223	5.5	796	4	US-08-961-083-56
4	204	5.0	763	4	US-08-961-083-66
5	168	4.1	708	4	US-09-131-648-2
6	167	4.1	1112	4	US-09-353-585-2
7	167	4.1	1112	4	US-09-353-585-3
8	160	3.9	968	4	US-09-180-439-3
9	160	3.9	968	4	US-09-180-439-4
10	159	3.9	799	4	US-09-180-439-6
11	155.5	3.8	359	1	US-08-303-238-4
12	155.5	3.8	359	4	US-08-458-834-4
13	153.5	3.8	603	1	US-08-190-802A-50
14	153.5	3.8	603	4	US-08-477-346-50
15	152.5	3.7	605	1	US-08-190-802A-49
16	152.5	3.7	605	4	US-08-477-346-49
17	152.5	3.7	980	2	US-08-473-553A-6
18	152.5	3.7	985	2	US-08-473-553A-2
19	151	3.7	806	4	US-08-945-983-2
20	151	3.7	863	2	US-08-666-271-2
21	150.5	3.7	353	6	5340934
22	150	3.7	1016	4	US-09-180-439-8
23	150	3.7	1091	3	US-08-986-485-5
24	149.5	3.7	342	1	US-08-272-919-2
25	149.5	3.7	342	1	US-08-619-916-2
26	149.5	3.7	342	1	PCT-US95-08542-2
27	149	3.7	605	4	US-09-063-950-5

**ALIGNMENTS**

RESULT 1  
PCT-US95-10509-2

; Sequence 2, Application PC/TUS9510509  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Priscilla  
; APPLICANT: Potter, Terry  
; APPLICANT: Sawyer, Richard  
; APPLICANT: Drevets, Douglas  
; TITLE OF INVENTION: INTERNALIN PRODUCTS AND PROCESSES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.A.  
; ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10509  
FILING DATE: 18 AUGUST 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kovarik, Joseph E.  
REGISTRATION NUMBER: 33,005  
REFERENCE NUMBER: 2879-11-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 746 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-10509-2

Query Match 7.9%; Score 322.5; DB 5; Length 746;  
Best Local Similarity 30.6%; Pred. No. 1.1e-16;  
Matches 92; Conservative 66; Mismatches 136; Indels 7; Gaps 4;

Qy 399 VIKLDLGSRK--DPLQRKGSLPLNLETIGIIFTPIKDIDSPVLQFKKLKQLMTRGVTD 456  
Db 2 ILKTVLGLKTNWDTVSQTDQVTTLOADRLG--IKSIDGLEYLNLTQINFNSNQLTD 58

QY 457 YRFELDNMPOLEGIDISONNLKDISFLSKVKNLTIVAAADNGIEDIRPLQLPNLKFVLS 516  
 Db 59 ITPLKLDTKLVDIIMNNNQIAIDITPLANLTNTGLTFLNNOITDIDPLKNLTLNRLELS 118  
 QY 517 NNKISDLSPLASLHQELHIDNNQITDLSPVSHKESLTVVDSLRSRNADVDTL-QAPKL 575  
 Db 119 SNTISDISALSGLTLNQQLSE-GNQVTDLKPLANLTTLERLDISSNKVSDisVLAKLTLN 177  
 QY 576 ETLMVNDTKVSHLDLKNNNPLSSLSINRAQLOSLEGIEASSVIVRVEAEGNQIKSLVL 635  
 Db 178 ESLIATNNQISDITPLGILTNLDELSLNQGNQLKDGTTLASLTNTDLDLANNQISNLAPL 237  
 QY 636 DKQGSLTFLDVIGNQNLTSLEGVNNTALDILSVSKNQLTNVNLSPKPKTVTNIDISHNNI 695  
 Db 238 SGLTKTELKGANQISNISPLLAGLTALTNELENQLEDISPISNLKNTLYLTYFNNI 297  
 QY 696 S 696  
 Db 298 S 298

RESULT 2  
 US-08-961-083-182  
 Sequence 182, Application US/08961083  
 Patent No. 6159469

GENERAL INFORMATION:  
 APPLICANT: Choi et. al.  
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
 NUMBER OF SEQUENCES: 452  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961, 083  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36, 373  
 REFERENCE/DOCKET NUMBER: PB340P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 182:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 447 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-961-083-182

Query Match 5.7%; Score 233; DB 4; Length 447;  
 Best Local Similarity 30.1%; Pred. No. 4.1e-10;  
 Matches 75; Conservative 36; Mismatches 96; Indels 42; Gaps 12;

Query Match 5.5%; Score 223; DB 4; Length 796;  
 Best Local Similarity 19.5%; Pred. No. 5.8e-09;  
 Matches 168; Conservative 116; Mismatches 279; Indels 300; Gaps 42;

QY 71 -DDGFILTKDSKLSKTDOGIVWDHDGHSHFIFYADLKG--SPFEYLIP---KGASL--- 121  
 Db 262 ESDGLVF-DPAKITISRTPNGVAIPGDHYHFTIPYSKLSALEEKIARMVPISGTGSTVSTN 320  
 QY 122 AKP-----AVAQRAASQGTSK-VADPHHYEFNPADTAEDALGYTVRHDDHFHYTL 172  
 Db 321 AKPNEVSSLLSLSNPSSLTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 380  
 QY 173 KSSLSGQTOAQKVATRLPQTSSLVSTATANGIPGLHFPTSDGEQENGQGIVGVTKDSI 232  
 Db 381 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH----EXHEEDGYGFDANRITAEDESGP 433  
 QY 233 LWDHDGHLH 241  
 Db 434 VMSHGDHNH 442

RESULT 3  
 US-08-961-083-56  
 Sequence 56, Application US/08961083  
 Patent No. 6159469

GENERAL INFORMATION:  
 APPLICANT: Choi et. al.  
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
 NUMBER OF SEQUENCES: 452  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961, 083  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36, 373  
 REFERENCE/DOCKET NUMBER: PB340P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 796 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-961-083-56

Query Match 5.5%; Score 223; DB 4; Length 796;  
 Best Local Similarity 19.5%; Pred. No. 5.8e-09;  
 Matches 168; Conservative 116; Mismatches 279; Indels 300; Gaps 42;

QY 30 TYPITKQSRKGMTSNKIKPIKKSKTKTHKGVAGVDFPTDDGFILTKDSKLSKTQG 89  
 Db 1 SYEGLYQARTVKENNRVSYIDGQATOKT-ENLTPDEVSKREG--INAEQIVIKITDQG 57  
 QY 90 IWDHDGHSHFIFYADLKGSPFEYLIPKGASLAKPAVAQRAASQGTSKVDAPHHYEFNP 149  
 Db 58 YVTSHGDHY-----YNGKVPYDAISEELL-----MKDP--NYKLKD 94

QY 150 ADIVAEDALGYTURHDDHFHYTLKSS-----LSGOTOAQAKOVATRLPOTSSLV 198  
 ||| | | | : | ; | | : | | : | | : |  
 Db 95 EDIVNEVKGGYVIKVKGKYYVLKDAAHADNVRTKEEINRQKQEHQSREGGTPRNDGA 154  
 QY 199 STATANGIPGLHFPSTDGFQFNQGQIVGVTKDSILVDHDGHLPISFADL----- 248  
 : | : | | : | | : | | : | | : |  
 Db 155 ALARSQG----RYTTDDGYIFNASDIEDTGDAYIVPHGDHYHYPKNELSASELAAA 210  
 QY 249 -----RQG-----GWAHVADQYDPAKKAEKPAETHQTPELSEREKEYQ 286  
 | |  
 Db 211 FLSGRGNLNSNSRTYRRQNSDNTSRTNW--VPSVSNPGTTNTNTNSNSQSNDID 268  
 QY 287 EKLAYL-----AEKLIGIDPSTIKRVETQDGKLGLEYPHDHAHVL--MLSDIE 332  
 | |  
 Db 269 SLLKQOLYKLPLSQRHESDGFLVFDPAI---TSRTARGVAVPHGHDHYHFTPYQSOMSEL 324  
 QY 333 --IGKDIP---DPHAI EHARELEKHKGMDTLRALGFDEEVILDIVRTHDAPTPFSNE 386  
 | | : | |  
 Db 325 ERARIILPLRYRSNHWVPSDRP-----EOPSPQPTPE 356  
 QY 387 KDPNMMKEWLATVIKLDLGSRKDPQRLQKGSLLPNL-ETLGIGFTPIKDISPVQLQFKKL 445  
 | | : | |  
 Db 357 PSPGPQP---APNLKIDSNS-----SLVSQLVRKVGEFY----- 387

Query Match 5.0%; Score 204; DB 4; Length 763;  
 Best Local Similarity 19.8%; Pred. No. 1.6e-07;  
 Matches 171; Conservative 125; Mismatches 314; Indels 254; Gaps 43;  
 Db 503 PLGQ---LPNL----KFLVLSNNKIDSLSPLASLHQQLQELHIDNNQITDLSPVSHKE 552  
 | |  
 Db 434 PRDQEFDYKAYNLTEAHKALFXNKGRNSDFQALDKL--LERLNDES-----TNKE 482  
 QY 553 SLTVWDLSRNADVLDLATQPKLETLMVNNDTKVSHLDLFLKNNPNLSSLSINRAQOSLEG 612  
 | |  
 Db 483 KL--VD-----DLAFLAP-----ITHPERL-GKPN----- 505  
 QY 613 TEASSVIVRVEAEGNQIQLVJLQGSILTFLDVGTGNQLTSLEGVNNFTALDILSVSKNQ 672  
 | |  
 Db 506 -----SQIEYTEDEVRIAQIADK-----YTSDGY-IFDEHDIISDEGDA 544  
 QY 673 LTNVNLSPKPNKTVTNDISH--NNISLADLKLNQHPEAIKN--FPAVYEGSMVGNG 727  
 | |  
 Db 545 YVTPHMGH-----SHWIGKDSLSD--KEVVAQAYTKEKGILPPSPDADVKANP 591  
 QY 728 TAAEKAMATAKESQAEESESHDYHNHNHTYEDEEGHA-----HEHRDK---DDHHH- 776  
 | | : | |  
 Db 592 TGDSAATAIYNRVKGKRIPLVRLPYMVEHTIVEVKNGNLIIIPHHDHYHNIKFAWFDDHTYK 651  
 QY 777 -----EHEDE 781  
 | | |  
 Db 652 APNGYTYLEDLFATIKYYVEHPDE 674

---

RESULT 4  
 US-08-961-083-66  
 Sequence 66, Application US/08961083  
 Patent No. 6159469  
 GENERAL INFORMATION:  
 APPLICANT: Choi et. al.  
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
 NUMBER OF SEQUENCES: 452  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961,083  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PB340P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 INFORMATION FOR SEQ ID NO: 66:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 763 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-961-083-66

QY 624 AEG-----NQIKS-----LVLKDKQGSL-----TFLDVTGNOL 651  
Db 584 AKGAEATYNRVKAKKVPLDRMPYNQVTVEVKNGSLIIPHVDHYHNIKEFWFD----- 637  
QY 652 TSLEGV---NNFTALDILSVSKNQLTNVNLSKPNTVTNIDISHNNNISLADLKNEQHI 707  
Db 638 ---EGLYEAPKGYLEDLLATKVYVVERPN-ERPHS-----DNGFGNA-----DHV 680  
QY 708 PEAIAKNFPFVYEGSMVNGT---AEEKAAMATKAKESAQEASESHD--YNHNHTYEDEE 762  
Db 681 QR--NKN----GOADTNQTEKPEEKPQSEKPEETPREEKPQSEKPEEE 732  
Db 733 SPEESEPQVETEKVEEKLREAED 756

RESULT 5  
US-09-131-648-2  
; Sequence 2, Application US/09131648  
; Patent No. 6168920  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Patterson, Chandra  
; TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS  
; FILE REFERENCE: PF-0576 US  
; CURRENT APPLICATION NUMBER: US/09/131,648  
; CURRENT FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PERL program  
; SEQ ID NO 2  
; LENGTH: 708  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 2687731  
; US-09-131-648-2

Query Match 4.1%; Score 168; DB 4; Length 708;  
Best Local Similarity 21.7%; Pred. No. 8.6e-05;  
Matches 113; Conservative 80; Mismatches 158; Indels 170; Gaps 24;

QY 380 TPPPSNEKDPPNMKEWLAVTKLDLGSRKDP-----LQRKGLSLLPNLET 425  
Db 88 TDFFPVNLTLGDLQLSQNLSSVTNINV-KKMPQLLSVYLEENKLTELPEKCLSELNLQEL 145

QY 426 GIGFTPPIKDISPVLQFKKLKOLL----MTKTGVTDYRFLDNMPQLEGIDISON--NLK 477  
Db 146 YINHHNLSTISPQ-AFTGLHNLRLHLNSRNLQMINNSKWFDALPNLEILMIGENPIIRK 204

QY 478 DISFLSKYKKNLTVAADN----GIEDIR----PLGQLPNLF 512  
Db 205 DMNFKPLINRLSLVIAGINLTELPDNALVGLENLNLESISFYDNRLLIKVPHVALQKVNLKF 264

QY 513 LVLSNNKISDL--SPLASLHQLOELHIDNNQ---ITDLSPVSHKESLTWVDSLNRADVDL 567  
Db 265 LDLNKPINRIRRGDFSNMLHLKELGINNMPELISIDS LAVDNLPDLRKIEATNNPRLSY 324

QY 568 ---ATLQAPKLETLMVNDTKVSHL--DFLKNNPNLSSLI-----NRA 605  
Db 325 IHPNAFFRLPKLESMLMLNSNALSALYHGTIESLSPNLKEISIHSNPICDCVIRWMNMKT 384

QY 606 QLOSLE-----GTEASSV----- 620  
Db 385 NIRFMEPDSDLFCVDPPEFOQONVRQVHERDMMEICLPLIAPESFPSNLSNVEAGSYVSFHC 444

QY 621 RVEAE-----GNOIQLSIVLKDQ---QGSLTFLDVTGNQLTSLEG-----VN 658  
Db 445 RATAEPOPEIYWITPSQQKLLPNTLTDKFVYHSEGT--LDING--VTPKEGGLYCIA 499

RESULT 6  
US-09-353-585-2  
; Sequence 2, Application US/09353585  
; Patent No. 6287865  
; GENERAL INFORMATION:  
; APPLICANT: Dixon, Mark S  
; Jones, David A  
; Jones, Jonathan DG  
; TITLE OF INVENTION: Plant pathogen resistance genes and uses  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye PC  
; STREET: 8th Floor, 1100 No. 6287865th Glebe Road  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/353,585  
; FILING DATE: 15-Jul-1999  
; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q 1/68  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/930,277  
; FILING DATE: 27-OCT-1997  
; APPLICATION NUMBER: PCT/GB96/00785  
; FILING DATE: 01-APR-1996  
; APPLICATION NUMBER: GB 9506658.5  
; FILING DATE: 31-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MS Mary J Wilson  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 620-69  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Tomato  
; STRAIN: Cf2  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
; US-09-353-585-2

Query Match 4.1%; Score 167; DB 4; Length 1112;  
Best Local Similarity 24.3%; Pred. No. 0.0002;  
Matches 104; Conservative 49; Mismatches 141; Indels 134; Gaps 20;

QY 396 LATVIKLDLGSRKDPQLQRKG----LSLLPNLETIGI-----GFTPIKDISSPVLOFKL 444

Db 118 LTNLVYLDLNNN---QISGTIPQQIGLLAKLQIRIFHNLNGFIP-KEIG-----YL 166 ; INFORMATION FOR SEQ ID NO: 3:  
 QY 445 KQLLMTKTGVTDYRFLDNMPQLEGIDISQNNLKDISFLSKYKN-----LT 489 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1112 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: <Unknown>  
 ; GENERAL INFORMATION:  
 ; TOPOLGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: YES  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Tomato  
 ; STRAIN: Cf2  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 ; US-09-353-585-3

QY 525 ---PLASLHQELHIDNNQITDLSPI-VSHKESLTVDLRSNA----DVDLATLQAPK 574  
 Db 279 IPASLGNLNLNSFLFLFLYGNQLSGSIPEEIGYLRLSLNVNLVNLNNL 338

QY 575 LETLMVNNDTKVSHLDFLKNNPNLSSL-----SINRAOLOSLLEGIEASSV 618  
 Db 339 RLNLVNNQNLGSIPASLGNLNLNSMLYLYNNQNLSGS 398 ; Query Match Score 167; DB 4; Length 1112;  
 ; Best Local Similarity 4.1%; Pred. No. 0.0002; Mismatches 141; Indels 134; Gaps 20;  
 ; Matches 104; Conservative 49; Mismatches 141; Indels 134; Gaps 20;  
 QY 619 IVRVEAEGNQIKSLVLDKQ----GSLTFLDVTGNQTLSL--EGVNNTALD 664  
 Db 399 IPASLGNLNLNSRLYLYNNQNLGSIPASLGNLNLNSMLYLYNNQNLSGS 458 ;  
 ;  
 QY 665 ILSVSKNQLTNVNLSPKN----KTVTNIDISH-----NNISLADLKNE- 704  
 Db 459 FFLFLYENQLAS---SVPPEEIGYLRLSLNVLDSENALNGSIPASFGNLLNL 515 ;  
 ;  
 QY 705 -QHIEPAI 711  
 Db 516 SGSSPEEI 523

RESULT 7 US-09-353-585-3 ;  
 ; Sequence 3, Application US/09353585  
 ; Patent No. 6287865  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dixon, Mark S  
 ; Jones, David A  
 TITLE OF INVENTION: Plant pathogen resistance genes and uses  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon & Vanderhye PC  
 STREET: 8th Floor, 1100 No. 6287865th Glebe Road  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: United States of America  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/353,585  
 FILING DATE: 15-Jul-1999  
 CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q 1/68

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/930,277  
 FILING DATE: 27-OCT-1997  
 APPLICATION NUMBER: PCT/GB96/00785  
 FILING DATE: 01-APR-1996  
 APPLICATION NUMBER: GB 9506658.5  
 FILING DATE: 31-MAR-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Ms Mary J Wilson  
 REGISTRATION NUMBER: 32,955  
 REFERENCE/DOCKET NUMBER: 620-69  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 816-4000  
 TELEFAX: (703) 816-4100

---

RESULT 8 US-09-180-439-3 ;  
 ; Sequence 3, Application US/09180439  
 ; Patent No. 6225532  
 ;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dixon, Mark S  
 ; APPLICANT: Hatzixanthis, Kostas  
 ; APPLICANT: Jones, David A  
 ; APPLICANT: Jones, Jonathan DG  
 ; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
 ; FILE REFERENCE: 620 - 53  
 ; CURRENT APPLICATION NUMBER: US/09/180,439  
 ; CURRENT FILING DATE: 1998-12-06  
 ;  
 ; EARLIER APPLICATION NUMBER: PCT/GB97/01249  
 ; EARLIER FILING DATE: 1997-05-08  
 ;  
 ; EARLIER APPLICATION NUMBER: GB 9609681.3  
 ; EARLIER FILING DATE: 1996-05-09  
 ; EARLIER APPLICATION NUMBER: GB 9619924.5  
 ; EARLIER FILING DATE: 1996-09-24  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 3  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: *Lycopersicon esculentum*  
US-09-180-439-3

; SEQ ID NO 4  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: *Lycopersicon esculentum*  
US-09-180-439-4

; SEQ ID NO 6  
; LENGTH: 799  
; TYPE: PRT  
; ORGANISM: *Lycopersicon esculentum*  
US-09-180-439-6

CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/978,931  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: KONSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: P-LA 9453  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

490 LVAADNGIEDIRP--LGQLPNLKFLVLSNNKISDLSP--LASLHQLOELHIDNNQITDL 545  
  : : | ; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
267 YLDLKENALNGSIPASLGNLNNLRLYLYNNQQLSGSIEEIGYLSSLTNLYLGNNSLIGL 326

Query Match 3.8%; Score 155.5; DB 1; Length 359;  
 Best Local Similarity 25.8%; Pred. No. 0.00029;  
 Matches 93; Conservative 51; Mismatches 101; Indels 115; Gaps 22;

Db	387	VLSMSSNSFSGELPSSIISNLTSKILDFFGRNNLEGAIPQCFGNISSLQVFDMMNNKLSGT	446
Qy	613	---IEASSVIVRVEAEGNQIKSLV--LKDKQGSLTFLDVGNQL--TSLEGVNNTALD	664
Db	447	LPTNEFISIGCSLISLNLLHGELEDEIPWSDLNDNCRKQLQVLDLGDNQLNDTFPMWLGLTPCLR	506
Qy	665	ILSVSKNQL-----TNVNLSPKPNKTVTNIDISHNNISLADLKLNEQHIEPAIAKNEPAV	718
Db	507	VLRLTSNKLHGPIRSSGAEIMFPDLRI--IDLSRNAFS-----QDLPTSLFEHL--	553
Qy	719	YEGSMVGNCTAEE	731
Db	554	-KGMRDVKTMEE	565
RESULT	11		
US-08-303-238-4			
; Sequence 4, Application US/08303238			
; Patent No: 5654270			

QY	443	KLKQLLMLTKTGVTDFRLDNMPLEGIDISONNLKDISFLSKYKNLTVAADNGIEDIR	502
Db	61	HLRVVOCSDLG-----LDKV-----KDLP-----PDTLLDQNKKITEIK	97
QY	503	--PLGQLPNLKFLVLNSNNKISDLSP--LASLHQELHIDNNQITDLSPVSHKESLTWVD	558
Db	98	DGDFKNLKNLHALILVNKNISKVSPGAFTPVLVKLERLYLSKNQELPEKMPK-----	150
QY	559	LSRNADVDLATLQAPKLETLMVNNDTKVSHLDF-----LKNNPNLSSLSINRAOLO	608
Db	151	-----TLQELRAHENET-----TKVRKVTFNGLNQMTIVIELGTNP-LKSSGIENGAFQ	197
QY	609	SLEGIEASSVVIRVEAEGNOIKSLVLDKQG----SLTFLDVTGNQLT----SLEGVNNE	660
Db	198	GMKKLS----YIRI-ADTN----ITSIPOGLPPSLTELHLDGNNKISRVDAAASLKGNNL	247
QY	661	TALDI-----LSVSKNQLTNV--NLSKPNKTVTNIDISHNNISL	697
Db	248	AKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAE-HKYIQVVLHNNNISV	306

APPLICANT: WHITBY, DAVID J.  
APPLICANT: HARPER, JOHN R.  
APPLICANT: PIERSCHBACHER, MICHAEL D.  
APPLICANT: BORDER, WAYNE A.  
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS  
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122

STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/458, 834  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/978, 931  
 FILING DATE: 17-NOV-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KONSKI, ANTOINETTE F.  
 REGISTRATION NUMBER: 34, 202  
 REFERENCE/DOCKET NUMBER: P-LA 9453  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-535-9001  
 TELEFAX: 619-535-8949  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 359 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ; US-08-458-834-4

Query Match 3.8%; Score 155.5; DB 4; Length 359;  
 Best Local Similarity 25.8%; Pred. No. 0.00029; Mismatches 101; Indels 115; Gaps 22;

Qy 397 ATVIKLDLG--SRKDPLQRKGL--SLLPNPLETLGIG-----FTPPIKDISPVLQFK---442  
 Db 3 ATIILLLLAQVSWAGPQFQORGFLDFMLEDASGIGPEVPDDRFDFEP--SLGPVCPCFRCQC 60  
 Qy 443 KLQLQMLMTKGTVTDYRFLDNNMPQLEGIDISONNLKDISFLSKYKNLTVAADNGIEDIR 502  
 Db 61 HLRWVQCSDLG-----LDKV-----KOLP-----PDTLQLDNKKITEK 97  
 Qy 503 --PLGLQPNLKFLVLSSNNKISDLSP--LASLHQLOELHIDNNQNITDLSPVSHKESLTWVD 558  
 Db 98 DGFDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKQNKEPEKMP-----150  
 Qy 559 LSRNADVDTLQAPKLETLMVNDTKVSHLDF-----LKNNPNLSSLSINRAQLO 608  
 Db 151 -----TQELRAHENET-----TKVRKVTFNGLNQMIVELGTNP-LKSSGIENGAFQ 197  
 Qy 609 SLEGIEASSVIVRVEAEGNQIKSLVKKDKQG---SLTFLDVTGNQLT----SLEGVNMF 660  
 Db 198 GMKKLS---YIRI-ADTN-----ITSIPQGLPPSITELHLDGNKISRVDAAASKGLNL 247  
 Qy 661 TALDI-----LSVSKNQLTNV--NLSKPNKTVTNIDISHNNISL 697  
 Db 248 AKLGLSFNSISAVDNGSLANTPHRELHLDNNKLTRVPGGLAE-HKYIQVWLHNNSV 306  
 RESULT 13  
 US-08-190-802A-50  
 Sequence 50, Application US/08190802A  
 Patent No. 5519003  
 GENERAL INFORMATION:  
 APPLICANT: Mochly-Rosen, Daria  
 APPLICANT: Ron, Dorit  
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
 TITLE OF INVENTION: Thereof  
 NUMBER OF SEQUENCES: 265  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dehlinger & Associates  
 STREET: P.O. Box 60850  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306-0850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/190, 802A  
 FILING DATE: 01-FEB-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fabian, Gary R.  
 REGISTRATION NUMBER: 33, 875  
 REFERENCE/DOCKET NUMBER: 8600-0139  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ ID NO: 50:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 603 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: insulin-like growth factor bind.  
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33  
 ; US-08-190-802A-50

Query Match 3.8%; Score 153.5; DB 1; Length 603;  
 Best Local Similarity 23.3%; Pred. No. 0.00089; Mismatches 174; Indels 91; Gaps 20;

Qy 296 LGIDPSTIKRVERTDGGKLGLLEYPHHDHAHVLMSDIEIGKDIIDPHAEARELEKHVG 355  
 Db 103 LNLOGSWLRSLEPQ-ALLGLQNLYYLHLERNRLRNLAVG-----LFTHTPSLASLSS 154  
 Qy 356 MDTLRALGDFEEVILDIVRTHDAPTPFPSSNEKDPNMMKKEWLATVIKLDLGSRK---DPL 411  
 Db 155 SNLGLRL--E EGLFOQLSHLWDLNLGWNSLWVLPDTVFOGLGNLHELVLAGNKLTYLQPA 212  
 Qy 412 ORKGGLSLLPNLETLGIGFTPKDISPVLFQKFLKQQLMKT---TGYTDYRFLDNMPQLEG 468  
 Db 213 LFCGGLGELRELDLSRNALRSVK-ANVFVHLPRQLYLDRLNLTAVAPGAFL-GMKALRW 270  
 Qy 469 IDISONNLKDT--SFLSKYKNLTVAADNGIEDIRP--LGOLPNLJKFLVLSNNKISDLS 524  
 Db 271 LDLSHNRVAGLMDFFPGLLGLHVRLAHNAIASLRPRFKDLHFLFELQGLGHNRQLG 330  
 Qy 525 -PLASLHQLOELHIDNNQITD--LSPVSHKESLTVVDSLNRNADVDTLQ-----APK 574  
 Db 331 ERTFEGLGQLEVTLNDNQITEVRVGFASGLFNVAVMNLSGNC--LRLSPERVFQGLDK 387  
 Qy 575 LETLMVNDTKVSHLD-----FLKNNPNLSSLSINRAQLOQSLEGIEASSVIVR 621  
 Db 388 LHSLHLEHSCLGHVRLHTFAGLGLRRFLRDN-----SISSIEEOSLAGL-----433  
 Qy 622 VEAEGNQIKSLVKKDKQSLTFLDVGTGNQLTLS-----EGVNNFTADDILSVKNQLTNV 676  
 Db 434 -----SELLELDLTNRUTHLPRQLFQGLGH--LEYLLSYNQLTTL 473  
 Qy 677 N--LSKPNKTVTNIDISHNNI-SLAD 699  
 Db 474 SAEVLGPLQRAFWLDISHNLETIAE 499  
 RESULT 14  
 US-08-477-346-50  
 Sequence 50, Application US/08477346  
 Patent No. 6262023  
 GENERAL INFORMATION:  
 APPLICANT: Mochly-Rosen, Daria  
 APPLICANT: Ron, Dorit  
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses



Mon Dec 3 07:54:18 2001

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Page 10

OY	521	SDLSP--LASLHQLOELHIDNNQITDLSPVSHK--ESLTWVDLSRNADVLATLQAPLE	576
Db	303	ASLRPRTFKDLHFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHN----QLOEVKAG	356
OY	577	TLM-VNDTKVSHL--DFLKNNPNLSSLSINRAQLOQSLEGIEASSVIVRVEAEG---NQI	629
Db	357	AFLGLTNVAVMNLSGNCLRNLPSEQVFRGLGKLHSLHLEG---SCLGRIRPHTFTGLSGL	412
OY	630	KSLVVLKDK-----QGSLTFLDVTGNQLTSL----EGVNNTALDIISVSKNQ	672
Db	413	RRLFLKDNGLVLGIEEOSLWGLAELLELDLTSNQLTHLPHRLFQGLGK--LEYILLSRNR	469
OY	673	LTNV--NLSKPNKTVTNIDISHNNI	695
Db	470	LAELPADALGPLQRAFWLDVSHNRL	494

GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: December 3, 2001, 07:22:19 ; Search time 370.05 seconds  
(without alignments)  
594.256 Million cell updates/sec

Title: US-09-645-835A-4  
Perfect score: 4080  
Sequence: 1 MKTKVILLVGLLSQLTL.....DHDHEHEDENEAKDEONHAD 792

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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1: /cgn2_6/ptodata/2/paa/PCITUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
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16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
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19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4080	100.0	792	1 PCT-US00-23417-4	sequence 4, Appli
2	4080	100.0	792	20 US-09-645-835-4	Sequence 4, Appli
3	4080	100.0	792	20 US-09-645-835A-4	Sequence 4, Appli
4	322.5	7.9	746	6 US-08-293-246-2	Sequence 2, Appli
5	297.5	7.3	1019	18 US-09-471-255-86	Sequence 86, Appli
6	293.5	7.2	1019	18 US-09-471-255-85	Sequence 85, Appli
7	292.5	7.2	1019	18 US-09-471-255-55	Sequence 55, Appli
8	292.5	7.2	1019	18 US-09-471-255-84	Sequence 84, Appli
9	292.5	7.2	1019	18 US-09-471-255-87	Sequence 87, Appli

ALIGNMENT

RESULT  
PCT-US00-23417-4  
; Sequence 4, Application PC/TUS0023417  
; GENERAL INFORMATION:  
; APPLICANT: Heinrichs, Jon  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Koenig, Scott  
; APPLICANT: Adamou, John E.  
; TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
; TITLE OF INVENTION: Vaccines  
; FILE REFERENCE: 469201-402  
; CURRENT APPLICATION NUMBER: PCT/US00/23417  
; CURRENT FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: U.S. 60/150,750  
; PRIOR FILING DATE: 1999-08-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 792  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
PCT-US00-23417-4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY 61 KGVAAGVDFPTDDGFILTKDSKILSKTDQGIVVDHDGHSHFTFYADLKGSPFEYLIPKGAS 120  
Db 61 KGVAAGVDFPTDDGFILTKDSKILSKTDQGIVVDHDGHSHFTFYADLKGSPFEYLIPKGAS 120

QY 121 LAKPAVAQRAASQGTSKVADPHHHYEFNPADIVADEALGYTVRHHDDHFHYILKSSLSGQT 180

Db 121 LAKPAVAQRAASQGTSKVADPHHHYEFNPADIVADEALGYTVRHHDDHFHYILKSSLSGQT 180

QY 181 QAOAQKVATRLPOTSSLVSTATANGIPGLHFTSDGFQFNGQGIVGVTKDSTLVHDGHL 240

Db 181 QAOAQKVATRLPOTSSLVSTATANGIPGLHFTSDGFQFNGQGIVGVTKDSTLVHDGHL 240

QY 241 HPISFADLROGGWAHVADQYDPACKPAEKPAETHQPELSEREKEYOEKLAYLAEKGIDP 300

Db 241 HPISFADLROGGWAHVADQYDPACKPAEKPAETHQPELSEREKEYOEKLAYLAEKGIDP 300

QY 301 STIKRVETQDGKLGLEYPHHDHAHVMLSDIEIGKDIPDPAHARELEKHKGMDTLR 360

Db 301 STIKRVETQDGKLGLEYPHHDHAHVMLSDIEIGKDIPDPAHARELEKHKGMDTLR 360

QY 361 ALGFDEEVILDIVRTHADTPFPSENKEWLATVIKLDLGSRKDPQORKGLSLLP 420

Db 361 ALGFDEEVILDIVRTHADTPFPSENKEWLATVIKLDLGSRKDPQORKGLSLLP 420

QY 421 NLETLGIGFTPPIKDISPVQLQFKKLKQOLLMTKTGVTDYRFLDNMPOLEGIDISONNLKD 480

Db 421 NLETLGIGFTPPIKDISPVQLQFKKLKQOLLMTKTGVTDYRFLDNMPOLEGIDISONNLKD 480

QY 481 FLSKYKNLTVAADNGIEDIRPLGQDNLKFLVLVSNNKISDLSPLASLHQELHIDN 540

Db 481 FLSKYKNLTVAADNGIEDIRPLGQDNLKFLVLVSNNKISDLSPLASLHQELHIDN 540

QY 541 QITDLSPVSHKESLTWVDSLRSNAADVDAVLATLQAPKLETLMVNNDTKVSHLDLFLKNPNLSSL 600

Db 541 QITDLSPVSHKESLTWVDSLRSNAADVDAVLATLQAPKLETLMVNNDTKVSHLDLFLKNPNLSSL 600

QY 601 SINRAQLOQSLEGIEASSVIVRVEAEQNOIQLVLSNNKISDLSPLASLHQELHIDN 660

Db 601 SINRAQLOQSLEGIEASSVIVRVEAEQNOIQLVLSNNKISDLSPLASLHQELHIDN 660

QY 661 TALDILSVSKNQLTNVNLSPKPNKTVNTIDISHNNISLADLKNEQHPEAIAKNFPAVE 720

Db 661 TALDILSVSKNQLTNVNLSPKPNKTVNTIDISHNNISLADLKNEQHPEAIAKNFPAVE 720

QY 721 GSVNGNTAEKAAMATAKAKESAQEASESHDYNHNHTYDEEGHAHEHRDKDDHHEHED 780

Db 721 GSVNGNTAEKAAMATAKAKESAQEASESHDYNHNHTYDEEGHAHEHRDKDDHHEHED 780

QY 781 ENEAKDEQNHA 792

Db 781 ENEAKDEQNHA 792

RESULT 2

US-09-645-835-4

; Sequence 4, Application US/09645835

; GENERAL INFORMATION:

; APPLICANT: Heinrichs, Jon

; APPLICANT: Johnson, Leslie S.

; APPLICANT: Koenig, Scott

; APPLICANT: Adamou, John E.

; TITLE OF INVENTION: Pneumococcal protein Homologs and Fragments for

; FILE REFERENCE: Vaccines

; CURRENT APPLICATION NUMBER: US/09/645, 835

; CURRENT FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: U.S. 60/150, 750

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4 LENGTH: 792

; TYPE: Pro

; ORGANISM: Streptococcus pyogenes  
US-09-645-835-4

Query Match 100.0%; Score 4080; DB 20; Length 792;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKTKKVILVGLLSQLTLIACOSRNGTYPPIKTQSRKGMTSNKIKPIKKTNKTH 60

QY 121 LAKPAVAQRAASQGTSKVADPHHHYEFNPADIVADEALGYTVRHHDDHFHYILKSSLSGQT 180

Db 121 LAKPAVAQRAASQGTSKVADPHHHYEFNPADIVADEALGYTVRHHDDHFHYILKSSLSGQT 180

QY 181 QAOAQKVATRLPOTSSLVSTATANGIPGLHFTSDGFQFNGQGIVGVTKDSTLVHDGHL 240

Db 181 QAOAQKVATRLPOTSSLVSTATANGIPGLHFTSDGFQFNGQGIVGVTKDSTLVHDGHL 240

QY 241 HPISFADLROGGWAHVADQYDPACKPAEKPAETHQPELSEREKEYOEKLAYLAEKGIDP 300

Db 61 KGVAAGVDFPTDDGFILTKDSKILSKTDQGIVWDHDGHSHFTFYADLKGSPFEYLIPKGAS 120

QY 301 STIKRVETQDGKLGLEYPHHDHAHVMLSDIEIGKDIPDPAHARELEKHKGMDTLR 360

Db 301 STIKRVETQDGKLGLEYPHHDHAHVMLSDIEIGKDIPDPAHARELEKHKGMDTLR 360

QY 361 ALGFDEEVILDIVRTHADTPFPSENKEWLATVIKLDLGSRKDPQORKGLSLLP 420

Db 361 ALGFDEEVILDIVRTHADTPFPSENKEWLATVIKLDLGSRKDPQORKGLSLLP 420

QY 421 NLETLGIGFTPPIKDISPVQLQFKKLKQOLLMTKTGVTDYRFLDNMPOLEGIDISONNLKD 480

Db 421 NLETLGIGFTPPIKDISPVQLQFKKLKQOLLMTKTGVTDYRFLDNMPOLEGIDISONNLKD 480

QY 481 FLSKYKNLTVAADNGIEDIRPLGQDNLKFLVLVSNNKISDLSPLASLHQELHIDN 540

Db 481 FLSKYKNLTVAADNGIEDIRPLGQDNLKFLVLVSNNKISDLSPLASLHQELHIDN 540

QY 541 QITDLSPVSHKESLTWVDSLRSNAADVDAVLATLQAPKLETLMVNNDTKVSHLDLFLKNPNLSSL 600

Db 541 QITDLSPVSHKESLTWVDSLRSNAADVDAVLATLQAPKLETLMVNNDTKVSHLDLFLKNPNLSSL 600

QY 601 SINRAQLOQSLEGIEASSVIVRVEAEQNOIQLVLSNNKISDLSPLASLHQELHIDN 660

Db 601 SINRAQLOQSLEGIEASSVIVRVEAEQNOIQLVLSNNKISDLSPLASLHQELHIDN 660

QY 661 TALDILSVSKNQLTNVNLSPKPNKTVNTIDISHNNISLADLKNEQHPEAIAKNFPAVE 720

Db 661 TALDILSVSKNQLTNVNLSPKPNKTVNTIDISHNNISLADLKNEQHPEAIAKNFPAVE 720

QY 721 GSVNGNTAEKAAMATAKAKESAQEASESHDYNHNHTYDEEGHAHEHRDKDDHHEHED 780

Db 721 GSVNGNTAEKAAMATAKAKESAQEASESHDYNHNHTYDEEGHAHEHRDKDDHHEHED 780

QY 781 ENEAKDEQNHA 792

Db 781 ENEAKDEQNHA 792

RESULT 3

US-09-645-835A-4

; Sequence 4, Application US/09645835

; GENERAL INFORMATION:

; APPLICANT: Heinrichs, Jon

; APPLICANT: Johnson, Leslie S.

; APPLICANT: Koenig, Scott

; APPLICANT: Adamou, John E.

; TITLE OF INVENTION: Pneumococcal protein Homologs and Fragments for

; FILE REFERENCE: Vaccines

; CURRENT APPLICATION NUMBER: US/09/645, 835

; CURRENT FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: U.S. 60/150, 750

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4 LENGTH: 792

; TYPE: Pro

TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
 TITLE OF INVENTION: Vaccines  
 FILE REFERENCE: 469201-493  
 CURRENT APPLICATION NUMBER: US/09/645, 835A  
 CURRENT FILING DATE: 2000-08-25  
 PRIORITY APPLICATION NUMBER: U.S. 60/150, 750  
 PRIORITY FILING DATE: 1999-08-25  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 792  
 TYPE: PRT  
 ORGANISM: Streptococcus pyogenes  
 US-09-645-835a-4

Query Match 100.0%; Score 4080; DB 20; Length 792;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTKKKVILVGLLSSQLTLIACQSRRGNGTYPITKQSRKGMTSNKIKPIKKKKTNKTH 60  
 Db 1 MTKKKVILVGLLSSQLTLIACQSRRGNGTYPITKQSRKGMTSNKIKPIKKKKTNKTH 60

Qy 61 KGVAGVDFPTDDGFILTKDSKILSKTDQGIWVDHDGHSHFIFYADLKGSPPFEYLIPKGAS 120  
 Db 61 KGVAGVDFPTDDGFILTKDSKILSKTDQGIWVDHDGHSHFIFYADLKGSPPFEYLIPKGAS 120

Qy 121 LAKPAVAQRAASQGTSKVADPHHYEFNPADIVADEDALGYTVRHHDFHFLKSSLSGQT 180  
 Db 121 LAKPAVAQRAASQGTSKVADPHHYEFNPADIVADEDALGYTVRHHDFHFLKSSLSGQT 180

Qy 181 QAQAKOVAATRLPOTSSLVSTATANGIPGLHFPTSDGQFQNGQGIVGVTKDSILVHDGHIL 240  
 Db 181 QAOAKOVAATRLPOTSSLVSTATANGIPGLHFPTSDGQFQNGQGIVGVTKDSILVHDGHIL 240

Qy 241 HPISFADLRQGGWAHVADQYDPAKKAEPATHQTPPELSEREKEYQEKLAYLAEKLGIDP 300  
 Db 241 HPISFADLRQGGWAHVADQYDPAKKAEPATHQTPPELSEREKEYQEKLAYLAEKLGIDP 300

Qy 301 STIKRVETODGKGLGLEYPHHDHAHVILMLS DIEIGKDIIDPHAEARELEKHKGMDTLR 360  
 Db 301 STIKRVETODGKGLGLEYPHHDHAHVILMLS DIEIGKDIIDPHAEARELEKHKGMDTLR 360

Qy 361 ALGFDEEVILDIVRTHADPTFFPSNEKDPMNKEWLATVIKLDLGSRKDPLQRKGSLLP 420  
 Db 361 ALGFDEEVILDIVRTHADPTFFPSNEKDPMNKEWLATVIKLDLGSRKDPLQRKGSLLP 420

Qy 421 NLETIGIGFTPIKDISPVLPQLQQKLLMTKGTVDFLDNMPOLEGIDISONNLKDIS 480  
 Db 421 NLETIGIGFTPIKDISPVLPQLQQKLLMTKGTVDFLDNMPOLEGIDISONNLKDIS 480

Qy 481 FLSKYKNLTVAADNGIEDIRPLGQLPNLKFVLNSNNKISDISPLASLHQELHIDNN 540  
 Db 481 FLSKYKNLTVAADNGIEDIRPLGQLPNLKFVLNSNNKISDISPLASLHQELHIDNN 540

Qy 541 QITDLSPVSHKESLTWVDSLRSRNADVDLATLOAPKLETLMVNDFKSHDLFKNNPNLSSL 600  
 Db 541 QITDLSPVSHKESLTWVDSLRSRNADVDLATLOAPKLETLMVNDFKSHDLFKNNPNLSSL 600

Qy 601 SINRAQOLQSLEGIEASSVIVRVEAEGNQIKSLVKDKQSLTFDVTGNQLTSLLEGVNFF 660  
 Db 601 SINRAQOLQSLEGIEASSVIVRVEAEGNQIKSLVKDKQSLTFDVTGNQLTSLLEGVNFF 660

Qy 661 TALDLISVSKNQLTNVNLSPKPNKTVTNIDISHNNISLADLKLINEOHIPEAIAKNFPAYE 720  
 Db 661 TALDLISVSKNQLTNVNLSPKPNKTVTNIDISHNNISLADLKLINEOHIPEAIAKNFPAYE 720

Qy 721 GSMVNGTAAEKAMATKAKESAQEASESHDYNHNHTYEDEECHAHEHRDKDDHHEHED 780  
 Db 721 GSMVNGTAAEKAMATKAKESAQEASESHDYNHNHTYEDEECHAHEHRDKDDHHEHED 780

Qy 781 ENEAKDEONHAD 792

RESULT 4  
 US-08-293-246-2  
 Sequence 2, Application US/08293246  
 GENERAL INFORMATION:  
 APPLICANT: Campbell, Priscilla  
 APPLICANT: Potter, Terry  
 APPLICANT: Sawyer, Richard  
 APPLICANT: Drevets, Douglas  
 APPLICANT: Freed, John  
 TITLE OF INVENTION: INTERNALIN PRODUCTS AND PROCESSES  
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sheridan Ross & McIntosh  
 STREET: 1700 Lincoln Street, 35th Floor  
 CITY: Denver  
 STATE: Colorado  
 COUNTRY: U.S.A.  
 ZIP: 80203

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC Compatible  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/293, 246

FILING DATE:  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Kovarik, Joseph E.  
 REGISTRATION NUMBER: 33,005  
 REFERENCE/DOCKET NUMBER: 2879-11

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303/863-9700  
 TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 746 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-293-246-2

Query Match 7.9%; Score 322.5; DB 6; Length 746;  
 Best Local Similarity 30.6%; Pred. No. 2.2e-15;  
 Matches 92; Conservative 66; Mismatches 136; Indels 7; Gaps 4;

Qy 399 VIKLDLGSRK--DPLQRKGSLLLPNLETLGIGFTPIKDISPVLPQLQFKKLQQLMKTGVTD 456  
 Db 2 ILKTVLGKTNVTDVTQDQVTLQADRLG--IKSIDLGEYLNLTQINFNNQLT 58

Qy 457 YRFLDNMPOLEGIDISONNLKDISFLSKYKNLTVAADNGIEDIRPLGOLPNLKFVL 516  
 Db 517 NNKISDLSPPLASLHQELHIDNNQITDLSPVSHKESLTWVDSLRSRNADVDLATL-QAPKL 575

Qy 59 ITPLKDLTKLVDILMNQNLQDITPLANLNTLGTFLNFNQITDPLKLNLTNL 118

Db 519 NNKISDLSPPLASLHQELHIDNNQITDLSPVSHKESLTWVDSLRSRNADVDLATL-QAPKL 575

Qy 576 ETLMVNDFKSHDLFKNNPNLSSLINRAQOLQSLEGIEASSVIVRVEAEGNQIKSLVK 635

Db 178 ESLIATNNQISDITPLGLTNLDELSLNGNQLDIGTLASLTNL 237

Qy 636 DKQGSLTFLDVGNQLTSLLEGVNFTALDLISVSKNQLTNVNLSPKPNKTVTNIDISHNNI 695

Db 238 SGLTKLTELKGANOQISNISPLAGLTALTNLNENQLEDISPISNLKNLTYLTLYFNNI 297

Qy 696 S 696

Db 298 S 298

---

RESULT 5

; Sequence 86, Application US/09471255

; GENERAL INFORMATION:

; APPLICANT: BIOCHEM PHARMA INC.

; APPLICANT: HAMEL, Jos e

; APPLICANT: BRODEUR, Bernard R.

; APPLICANT: PINEAU, Isabelle

; APPLICANT: MARTIN, Denis

; APPLICANT: RIOUX, Clément

; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS

; FILE REFERENCE: 12806-11PCT

; CURRENT APPLICATION NUMBER: US/09/471, 255

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 60/113, 800

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 102

SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 86

; LENGTH: 1019

; TYPE: PRT

; ORGANISM: S. pneumoniae

US-09-471-255-86

Query Match

Best Local Similarity 7.38; Score 297.5; DB 18; Length 1019;

Matches 185; Conservative 114; Pred. No. 3.2e-13; Mismatches 286; Indels 277; Gaps 44;

Qy 16 SOLTLLIACOSRGNQTYPIKTKQRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT----- 70

Db 217 SOLSYSSTASDNN----TQSVAKGSTS--KPANKSENQSLKLKE--YDSPAORYS 265

Qy 71 -DDGFLITKDKSKLISKTDQGVIVDHGDGHSHFIFYADLKG--SPEFEYLIP--KCA 121

Db 266 ESDGLVF-DPAKIIISRTPNGVAIPHGDHYHFIPIYSKLSALEEKIARRVPIISGTGSTVSTN 324

Qy 122 AKP-----AVAQRAASQGTSK-VADPHHYEFNPADIVAEDALGYTVRHDDHFHY 172

Db 325 AKPNEVWSSLGSLSNPNSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHRGDHFHY 384

Qy 173 KSSLGSGTQAQAKQVATRLPOTSSLVSTATANGIPGLHFP-TSDGFOFNGQGIVGVTKDSI 232

Db 385 KSNQIGQPTLPPNNSLAT--PSPLPINPGTSH---EKHEEDGYGFANR TIAEDESGF 437

Qy 233 LVDHDGHLHPIASFADLROQGWAAHVADQYDPAKKAEPKAETHQT----- 275

Db 438 VMSHGHDHNHYFFKKDLTE-----EQIKAQKHLLEEVTSHNGLDSLSSHEQDYPSS 487

Qy 276 --PELSEREKEYQEKLAYLAEKGIDPSTIKRVETODKGKLGLEYPHHDHAHVLMLSDI 333

Db 488 NAKEMKOLDKKIEEKIAGIMQYGVKRESI--VWNKEKNAIYPHGDH----- 533

Qy 334 GKDIPIPDAEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPEPSNE---KD 388

Db 534 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 567

Qy 389 PNMM--KEWLATVIKLDLGSRKDPQLQRKGSSLNPLETLLGIGFTPIKDISPVLQFKKLQ 446

Db 568 GNKVYTGEELTNVNL---LKNSTFNQNFTLANGQKRVSFSPPELE-----KKLGI 617

Qy 447 LIMTKTGTQTYRFELD-----NMFOLEG---IDISONNLKDISFLS 483

Db 618 NMLVKLITPDGKVLEKVGKVFGEGVGNIANFELDQPYLPQTFKYTIASKDYPESYDG 677

Qy 484 KYKNLTLVA-----AADNGIEDIRPLGOLP-NLKFLY-----LSNN 518

Db 678 TFTVPTSLAYKMASQTIYFPFHAGDTYLR-VNPQFAVPKGTDALVVRDEFHGNAYLENN 736

Qy ~ 519 -KSDLS-PLASLHQ-----LQELHDNNQ--ITDLSPVSHKESLTWVDLS 560

---

RESULT 6

US-09-471-255-85

; Sequence 85, Application US/09471255

; GENERAL INFORMATION:

; APPLICANT: BIOCHEM PHARMA INC.

; APPLICANT: HAMEL, Jos e

; APPLICANT: BRODEUR, Bernard R.

; APPLICANT: PINEAU, Isabelle

; APPLICANT: MARTIN, Denis

; APPLICANT: RIOUX, Clément

; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS

; FILE REFERENCE: 12806-11PCT

; CURRENT APPLICATION NUMBER: US/09/471, 255

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 60/113, 800

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 102

SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 85

; LENGTH: 1019

; TYPE: PRT

; ORGANISM: S. pneumoniae

US-09-471-255-85

Query Match

Best Local Similarity 7.28; Score 293.5; DB 18; Length 1019;

Matches 188; Conservative 112; Pred. No. 6.5e-13; Mismatches 278; Indels 291; Gaps 46;

Qy 16 SOLTLLIACOSRGNQTYPIKTKQRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT----- 70

Db 217 SOLSYSSTASDNN----TQSVAKGSTS--KPANKSENQSLKLKE--YDSPAORYS 265

Qy 71 -DDGFLITKDKSKLISKTDQGVIVDHGDGHSHFIFYADLKG-SPEFEYLIP--GASL- 121

Db 266 ESDGLVF-DPAKIIISRTPNGVAIPHGDHYHFIPIYSKLSALEEKIARRVPIISGTGSTV 322

Qy 122 -AKP-----AVAQRAASQGTSK-VADPHHYEFNPADIVAEDALGYTVRHDDHFHY 170

Db 323 TNKPEVWSSLGSLSNPNSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHRGDHFHY 382

Qy 171 ILLSSLSGSGTQAQAKQVATRLPOTSSLVSTATANGIPGLHFP-TSDGFOFNGQGIVGV 228

Db 383 IPKSNOIGQPTLPPNNSLAT--PSPLPIN-----PGISHEKEEDGYGFANR TIAED 433

Qy 229 KDSILVDHDGHLHPIASFADLROQGWAAHVADQYDPAKKAEPKAETHQT----- 275

Db 434 ESGFIMSHGNHNYFFKKDLTE-----EQIKAQKHLLEEVTSHNGLDSLSSHEQ 483

Qy 276 --PELSEREKEYQEKLAYLAEKGIDPSTIKRVETODKGKLGLEYPHHDHAHVLMLSD 329

Db 484 DYPGNAKEMKOLDKKIEEKIAGIMQYGVKRESI--VWNKEKNAIYPHGDH----- 533

QY 330 DIEIGKDIPDPHAIHARELEHKH-VGMDTLRALGFDEEVILDIVRTHADPTPFPNSNE-- 386  
Db 534 -----IHADPIDEHKPYVG-----IGHSHSNYELFKPEEGV 563  
QY 387 --KDPNMM--KEWLATVIKLDLGSRKDPLQRKGSLSLPNLETLGIGFTPPIKDISPVLOFK 442  
Db 564 AKKEGNKVVYTGEELTNVNL--LKNSTFNQNFTLANGQKRVSFSPPELE-----K 613  
QY 443 KLKQLLMKTGTVDYRFLD-----NMPOLEG---IDISQNNLKDI 479  
Db 614 KLGGINMLVKLITPDGKVLEKVGKVFGEGVGNIANFELDQPYLPQGOTFKYTIAKDYPEV 673  
QY 480 SFLSKYKVNLTTLVA-----AADNGIEDIRPLGQLP-NLKFLV----- 514  
Db 674 SYDGTFVTPLSLAYKMASQTIFFYFPFHAGDTYL-RVNQFAVPKGTDALVRVFDEFHGNAY 732  
QY 515 LSNN-KISDLS-PLASLHQ-----LQELHIDNNO--ITDLSPVSHKESLT 556  
Db 733 LENNYKVEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT- 790  
QY 557 VDLRSRNADVTLQAPKLETLMVNNDTKVSHLDLFLKNNPN-LSSLSINRAQLQSL--EGI 613  
Db 791 -----DKPSILPQFKRNKAQENSKLDEKV 814  
QY 614 EASSVIVRVEAE----GNOQIKSLVLKD-----KQGSLTFLDVIG---NOLTSLEGV 657  
Db 815 EEPKTSEKVEKEKLSETGNSTNSTLEEVPVQEKVAKFAESYGMKLENVLNFNMDG- 873  
QY 658 NNFTALDILSVSKNQLTNVNLSPKPNKTVTNIDISHNNNISLADLKLNEQHIEPAIAKNFPA 717  
Db 874 -----TIELYLPSGEV---IKKN--MADE---TGEAPQGNGENKPS 906  
QY 718 VYEGSMVNGNTAEEKAAMATKAKESAQEA 746  
Db 907 --ENGKVSTGTVENQPT-ENKPADSLEA 932

RESULT 7

; Sequence 55, Application US/09471255  
; GENERAL INFORMATION:  
; APPLICANT: BIOCHEM PHARMA INC.  
; APPLICANT: HAMEL, Jos,e  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: PINEAU, Isabelle  
; APPLICANT: MARTIN, Denis  
; APPLICANT: RIOUX, Cl,ment  
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
; FILE REFERENCE: 12806-11PCT  
; CURRENT APPLICATION NUMBER: US/09/471, 255  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/113, 800  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 55  
; LENGTH: 1019  
; TYPE: PRT  
; ORGANISM: S. pneumoniae  
; US-09-471-255-55

Query Match 7.2%; Score 292.5; DB 18; Length 1019;  
Best Local Similarity 21.4%; Pred. No. 7.8e-13;  
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

QY 16 SQLTLIACQSRRGNGTYPPIKTKQSRKGMTSNKIKPIKKSKKNTKTHKGVAGVDFPT---- 70  
Db 217 SQLSYSSTSADNN-----TOSVAKGSTS--KPANKSENQSLKL--YDSPSAQRY S 265  
QY 71 -DDGFILTKDSKILSKTDQGIWVHDHGHSIFIYADLKG--SPFEYLIP--KGASL-- 121  
Db 266 ESDGLVF-DPAKIIISRTPNGVAVPHGDHYFIPYSKLSALEEKIARMVPISGTGSTVSTN 324

QY 122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVADEALGYTVRHDDHFHYIL 172  
Db 325 AKPNEVSSLGSLSSNPPSLLTISKELSSASDGYTFNPKDIVEETATAVIVRHGDHFHYIP 384  
QY 173 KSSLSGOTOAQAKQVATRLPQTSVLSTATANGIPLGLHFPTSDGFQFNGQGIVGVTKDSI 232  
Db 385 KSNOIQGPTLPNNSLAT--PSPSLPINPGTSH---EKHEEDGYGFEDANRIIAEDESGF 437  
QY 233 LVDHDGHLLHPISFADLRQGGWAHVADQYDPAAKKAEPATHQT----- 275  
Db 438 VMSHGDNHNYFFKKDLTE-----EQIKAAQKHLEVKTSHNGLDSLSSHEQDYPG 487  
QY 276 --PELSEREKEYQEKLAYLAEKLIDPSTIKRKRVTODGKLGLEYPHDHAHVMLSDIEI 333  
Db 488 NAKEMKDLKKIEKLKAGIMQYGVKRESI--VWNKEKNALIYPHGDH----- 533  
QY 334 GKDIPDPHAIHARELEHKH-VGMDTLRALGFDEEVILDIVRTHADPTPFPNSNE---KD 388  
Db 534 -----HHADPIDEHKPYVG----- 534  
QY 389 PNMM--KEWLATVIKLDLGSRKDPLQRKGSLSLPNLETLGIGFTPPIKDISPVLOFKKLQ 446  
Db 568 GNKVYTGEELTNVNL--LKNSTFNQNFTLANGQKRVSFSPPELE-----KKLGI 617  
QY 447 LLMTKTGVTYRFLD-----NMPOLEG---IDISQNNLKDISFLS 483  
Db 618 NMLVKLITPDGKVLEKVGKVFGEGVGNIANFELDQPYLPQGOTFKYTIAKDYPEVSYDG 677  
QY 484 KYNLTTLVA-----AADNGIEDIRPLGQLP-NLKFLV----- 518  
Db 678 TFTVPTSLAYKMASQTIFFYFPFHAGDTYL-RVNQFAVPKGTDALVRVFDEFHGNAYLENN 736  
QY 519 -KISDLS-PLASLHQ-----LQELHIDNNO--ITDLSPVSHKESLT 560  
Db 737 YKVGEEKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT----- 790  
QY 561 RNADVTLQAPKLETLMVNNDTKVSHLDLFLKNNPN-LSSLSINRAQLQSL--EGIEASS 617  
Db 791 -----DKPSILPQFKRNKAQENSKLDEKVVEPK 818  
QY 618 VIVRVEAE----GNOQIKSLVLKD-----KQGSLTFLDVIG---NOLTSLEGVNFT 661  
Db 819 TSEKVEKEKLSETGNSTNSTLEEVPVQEKVAKFAESYGMKLENVLNFNMDG----- 873  
QY 662 ALDILSVSKNQLTNVNLSPKPNKTVTNIDISHNNNISLADLKLNEQHIEPAIAKNFPAVYEG 721  
Db 874 -----TIELYLPSGEV---IKKN--MADE---TGEAPQGNGENKPS--EN 908  
QY 722 SMVNGNTAEEKAAMATKAKESAQEA 746  
Db 909 GKVSTGTVENQPT-ENKPADSLEA 932

RESULT 8

; Sequence 84, Application US/09471255  
; GENERAL INFORMATION:  
; APPLICANT: BIOCHEM PHARMA INC.  
; APPLICANT: HAMEL, Jos,e  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: PINEAU, Isabelle  
; APPLICANT: MARTIN, Denis  
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
; FILE REFERENCE: 12806-11PCT  
; CURRENT APPLICATION NUMBER: US/09/471, 255  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/113, 800  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 84

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; LENGTH: 1019
; TYPE: PRT
; ORGANISM: S. pneumoniae
US-09-471-255-84

Query Match          7.2%; Score 292.5; DB 18; Length 1019;
Best Local Similarity 21.4%; Pred. No. 7.8e-13;
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;
Db 217 SQLSYSSTASDNN-----TQSVAKGSTS--KPANKSENLQSLKEL-YDSPAQRYS 265

QY 71 -DDGFLITKDSKILSKTDQGIIVVDHDGHSHFTFYADLKG--SPFEYLIP--KGASL-- 121
Db 266 ESDGLVF-DPAKILSRTPNGVAIPHGDHYHFIPIYSKLSALEEKIARMVPIISGTGSTVSTN 324

QY 122 AKP-----AVAQRAASQTSK-VADPHHHYEENFPADIVAEDALGYTVRHDDHFHYTL 172
Db 325 AKPNEVSSLGSLSNNPSLTTSKELSSASDGYIFNPKDIVETATAYIVRHGDHFHYIP 384

QY 173 KSSLSGOTQAQAKQVATRLPOTSSLVSTATANGIPGLHFPTSDGFQFNGQGIVGVTKDSI 232
Db 385 KSNQIGQOPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFDANRRIADESGF 437

QY 233 LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEPETHQT----- 275
Db 438 VMSHGHDHNHYFFKKDLTE-----EQIKAQKHLEEVKTSHNGLDSLSSHEQDYS 487

QY 276 -PELSEREKEYQEKLAYLAEKGIDPSTIKRVETQDGKLGLEYPHHDHAHVMLSDIEI 333
Db 488 NAKEMKDLKKIEEKIAGIMQYGVKRESI---VVNKEKNAILYPHGDH----- 533

QY 334 GKDIIDPHATEHARELEHK--VGMDTLRALGFDEEVILDIVRTHADPTPPSNE---KD 388
Db 534 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 567

QY 389 PNMM--KEWLATVIKLDGSRKDPLQRKGGLSLLPNLETLGIGFTPIKDISPVLFKKLKQ 446
Db 618 GNKVYTGEELTNVVNL--LKNSTENNQNF'TLANGQKRVSFSEPPLE-----KKLGI 617

QY 447 LLMTKTVGTDYRFLD-----NMPOLEG---IDISONNLKDISFLS 483
Db 678 NMLVKLITPDGKVLEKVGKVFEGGVGNIANFELDQPYLPQGQTFKYTIASKDYPEVSYDG 677

QY 484 KYKNLTLVA-----AADNGIEDIRPLGQLP-NLKFLV-----LSNN 518
Db 737 YKVGEIKLPIPKLNQGTTAGNKIPVTFMANAYLDNOSTIVEV-PILEKENQT---- 790

QY 561 RNADVDTLQAPKLETLMVNDTKVSHLDFLKNNPN-LSSLSINRAQLQSL--EGIEASS 560
Db 791 -----DKPSILPQFKRNKAQENSKFDEKEVEPK 818

QY 618 VIVRVEAE-----GNOIKSLVLKD-----KQGSLTFLDWVG----NQLTSLEGVNNT 661
Db 819 TSEKVEKEKLSSETGNSTSNTSLEEVTWDVQEVKAFAESYGMKLENVLNFMDG---- 873

QY 662 ALDILSVSKNQLTNVNLSPKPKTVNIDISHNNISLADLKLNQHPEAIKNFPAVYEG 721
Db 874 -----TIELYLPSEGV---IKNN--MADF---TGEAPOQNGENKPS--EN 908

QY 722 SMVGNGTAAEKAAMATKAKESAQEA 746
Db 909 GKVSTGTVENQPT-ENKPADSLPEA 932

RESULT 9
US-09-471-255-87

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; Sequence 87, Application US/09471255
; GENERAL INFORMATION:
; APPLICANT: BIOCHEM PHARMA INC.
; APPLICANT: HAMEL, Jos-e
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: PINEAU, Isabelle
; APPLICANT: MARTIN, Denis
; APPLICANT: RIOUX, Clment
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/471, 255
; CURRENT FILING DATE: 1999-12-23
; PRIORITY NUMBER: US 60/113, 800
; PRIORITY FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 87
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: S. pneumoniae
US-09-471-255-87

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```

; Sequence 87, Application US/09471255
; GENERAL INFORMATION:
; APPLICANT: BIOCHEM PHARMA INC.
; APPLICANT: HAMEL, Jos-e
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: PINEAU, Isabelle
; APPLICANT: MARTIN, Denis
; APPLICANT: RIOUX, Clment
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/471, 255
; CURRENT FILING DATE: 1999-12-23
; PRIORITY NUMBER: US 60/113, 800
; PRIORITY FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 87
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: S. pneumoniae
US-09-471-255-87

```

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```

; Sequence 87, Application US/09471255
; GENERAL INFORMATION:
; APPLICANT: BIOCHEM PHARMA INC.
; APPLICANT: HAMEL, Jos-e
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: PINEAU, Isabelle
; APPLICANT: MARTIN, Denis
; APPLICANT: RIOUX, Clment
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/471, 255
; CURRENT FILING DATE: 1999-12-23
; PRIORITY NUMBER: US 60/113, 800
; PRIORITY FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 87
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: S. pneumoniae
US-09-471-255-87

```

---

QY 618 VIVRVEAE----GNOIQLVLD----KOGSLTFLDVIG---NQLTSLEGVNFT 661  
Db 819 TSEKEKEKLSETGNSTSNTLEEVPVDVQEVKAFAESYGMKLENLFNMDG---- 873  
QY 662 ALDILSVSKNQLTNVLNLSPNKTVTNIDISHNNISLADLKLNQEHTPEIAKNFPAVYEG 721  
Db 874 -----TIELYLPSGEV---IKNN--MADE---TGEAPOQNGENKPS--EN 908  
QY 722 SMVGNGTAEEKAAMATKAKESAQEA 746  
Db 909 GKVSTGTVENQPT-ENKPADSLPEA 932

RESULT 10  
US-09-471-255-88  
; Sequence 88, Application US/09471255  
; GENERAL INFORMATION:  
; APPLICANT: BIOCHEM PHARMA INC.  
; APPLICANT: HAMEL, Jos,<sup>e</sup>  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: PINEAU, Isabelle  
; APPLICANT: MARTIN, Denis  
; APPLICANT: RIoux, Cl,ment  
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
; FILE REFERENCE: 12806-11PCT  
; CURRENT APPLICATION NUMBER: US/09/471, 255  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/113, 800  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 88  
; LENGTH: 1019  
; TYPE: PRT  
; ORGANISM: S. pneumoniae  
; US-09-471-255-88

Query Match 7.2%; Score 292.5; DB 18; Length 1019;  
Best Local Similarity 21.4%; Pred. No. 7.8e-13;  
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

QY 16 SQLTLIACQSRGNNTYPIKTKQSRGMITSNKIKPIKKSKTKNTHKGVAGVDFPT---- 70  
Db 217 SQLSYSSTASDNN-----TOSVAKGSTS---KPANKSENLQLSLKEL--YDSPSAORYS 265  
QY 71 -DDGFLITKDKSKILSKTDQGIVVHDHGHSHEIFYADLKG--SPFEYLIP---KGASL-- 121  
Db 266 ESDGLVF-DPAKIIISRTPNGVAIPHGDHYFIPYSKLSALEEKIARMVMPISGTGSTVSTN 324  
QY 122 AKP-----AVAQRAASQGTSK-VADPHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172  
Db 325 AKPNEVVSSLGSLSSNPSSLTSSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 384  
QY 173 KSSLSGQTOQAQKQVATRLPOTSSLVSTATANGIPGLHFTPDSGFQFNGQGIVGVTKDSI 232  
Db 385 KSNOIQGQPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFEDANRITAEDESGF 437  
Qy 233 LVDHDGHLHPISFADLROQGWVADQYDPAKKAEPATHOT----- 275  
Db 438 VMSHGDHNHYFFKKDLTE-----EQIKAQKHLLEEVKTSHNGLDSLSSHEQDYP 487  
Qy 276 --PELSEREKEYQEKLAYLAEKGIDPSTIKRVETQDGKLGLEYPHDHAVHVLMLSDIEI 333  
Db 488 NAKEMKDLKKIEEKIAGIMKQYGVKRESI---WVNKEKNATYPHGDH----- 533  
Qy 334 GKDIPDPHAEHARELEKHK-VGMDTLRALGFDEEVLDIVRTHADTPFPNSNE---KD 388  
Db 534 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 567  
Qy 389 PNMM--KEWLATVIKDLGSRRKDPLQRKGSLLLPNLETLGIGFTPIKDISPVLOFKKLQ 446

Db 568 GNKVYTGEELTNVNL---LNSTFNQNFTLANGQKRVSFSPPELE-----KKLGI 6177  
QY 447 LLMTKTGVTDRFLD-----NMPOLEG---IDISONNLKDISFLS 4833  
Db 618 NMLVKLITPDGKVLEKVGKVFEGVGNIANFELDQPYLPQTFKYTIASKDYPPEVSYDG 6777  
QY 484 KYKNLTVA-----AADNGIEDIRPLQGP-NLKFLV-----LSNN 5188  
Db 678 TFTVPTSLAYKMASQTIFYPFHAGDTYLR-VNPQFAVPKGTDALVRVDEFHGNAYLENN 7366  
QY 519 -KISDLS-PLASLHQ-----LQELHDNQ--ITDLSPVSHKESLTWVDSL 5600  
Db 737 YKVGEIKLPIPKLNQGTTRTAGNKPVTMANYLDNQSTTYIVEV-PILEKENQT---- 7900

QY 561 RNADVDTLATLQAPKLETLMVNNDTKVSHLDNFLKNNPN-LSSLSINRAQOLSL--EGIEASS 6177  
Db 791 -----DKPSILPQFKRNKAQENSKFDEKVEEPK 818  
QY 618 VIVRVEAE----GNOIQLVLD----KOGSLTFLDVIG---NQLTSLEGVNFT 661  
Db 819 TSEKEKEKLSETGNSTSNTLEEVPVDVQEVKAFAESYGMKLENLFNMDG---- 873  
QY 662 ALDILSVSKNQLTNVLNLSPNKTVTNIDISHNNISLADLKLNQEHTPEIAKNFPAVYEG 721  
Db 874 -----TIELYLPSGEV---IKNN--MADE---TGEAPOQNGENKPS--EN 908  
QY 722 SMVGNGTAEEKAAMATKAKESAQEA 746  
Db 909 GKVSTGTVENQPT-ENKPADSLPEA 932

RESULT 11  
US-09-471-255-89  
; Sequence 89, Application US/09471255  
; GENERAL INFORMATION:  
; APPLICANT: BIOCHEM PHARMA INC.  
; APPLICANT: HAMEL, Jos,<sup>e</sup>  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: PINEAU, Isabelle  
; APPLICANT: MARTIN, Denis  
; APPLICANT: RIoux, Cl,ment  
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
; FILE REFERENCE: 12806-11PCT  
; CURRENT APPLICATION NUMBER: US/09/471, 255  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/113, 800  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 89  
; LENGTH: 1019  
; TYPE: PRT  
; ORGANISM: S. pneumoniae  
; US-09-471-255-89

Query Match 7.2%; Score 292.5; DB 18; Length 1019;  
Best Local Similarity 21.4%; Pred. No. 7.8e-13;  
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

QY 16 SQLTLIACQSRGNNTYPIKTKQSRGMITSNKIKPIKKSKTKNTHKGVAGVDFPT---- 70  
Db 217 SQLSYSSTASDNN-----TOSVAKGSTS---KPANKSENLQLSLKEL--YDSPSAORYS 265  
QY 71 -DDGFLITKDKSKILSKTDQGIVVHDHGHSHEIFYADLKG--SPFEYLIP---KGASL-- 121  
Db 266 ESDGLVF-DPAKIIISRTPNGVAIPHGDHYFIPYSKLSALEEKIARMVMPISGTGSTVSTN 324  
QY 122 AKP-----AVAQRAASQGTSK-VADPHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172  
Db 325 AKPNEVVSSLGSLSSNPSSLTSSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 384  
QY 173 KSSLSGQTOQAQKQVATRLPOTSSLVSTATANGIPGLHFTPDSGFQFNGQGIVGVTKDSI 232  
Db 385 KSNOIQGQPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFEDANRITAEDESGF 437  
Qy 233 LVDHDGHLHPISFADLROQGWVADQYDPAKKAEPATHOT----- 275  
Db 438 VMSHGDHNHYFFKKDLTE-----EQIKAQKHLLEEVKTSHNGLDSLSSHEQDYP 487  
Qy 276 --PELSEREKEYQEKLAYLAEKGIDPSTIKRVETQDGKLGLEYPHDHAVHVLMLSDIEI 333  
Db 488 NAKEMKDLKKIEEKIAGIMKQYGVKRESI---WVNKEKNATYPHGDH----- 533  
Qy 334 GKDIPDPHAEHARELEKHK-VGMDTLRALGFDEEVLDIVRTHADTPFPNSNE---KD 388  
Db 534 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 567  
Qy 389 PNMM--KEWLATVIKDLGSRRKDPLQRKGSLLLPNLETLGIGFTPIKDISPVLOFKKLQ 446

QY 173 KSSLSGOTQAQAKOVATRLPQTSSLVSTATANGIPGLHFPTSDGFFQFNGQGIVGVTKDSI 232  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 385 KSNQIGOPTLPNNSLAT--PSPSLPINPGTSH---EKHEEDGYGF DANR IAEDESGF 437  
 QY 233 LVDHDGHHLHPIASFADLRLQGGWAHVADQYDPAKKAEKPAETHQ--- 275  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 438 VMSHGDNHYFFKKDLTE----EQIKAQKHL EEVKTSHNGLDSLSSHEQDYP S 487  
 QY 276 --PELSEREKEYQEKLAYLAEKGIDPSTIKRVETQDGKLGLEYPHHDHAHVIMLDIEI 333  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 488 NAKEMKLDKKIEEKIAGIMKOYGVKRESI--VVNEKEKNATIYPHGDH-- 533  
 QY 334 GKDIPDPHAI EHARELEKH -VGMDTLRALGFDEEVILDIVRTHADTPFPNSNE---KD 388  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 534 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 567  
 QY 389 PNMM--KEWLATVIKLDLGSRKDPQLRKGLSLLPNLETLGIGFTPIKDISPVLQFKKLQ 446  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 568 GNKVYTGEELTNVNL--LNNSTFNQNFTLANGQKRVSFSPPELE-----KLG 617  
 QY 447 LLMTKGTVDYRFLD-----NMPQLEG---IDISQNNLKDISFLS 483  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 618 NMLVKLITPDGKVLEKVGKVFGEVGNTIANFELDQPYLPQTFKYTIASKDYPEVSYD 677  
 QY 484 KYKNLTLV A-----AADNGIEDIRPLGQLP-NLKFLV-----LSNN 518  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 678 TFTVPTSLAYKMASQTIFYPFHAGDTYL R-VNPQFAVPKGTDALVRVDEFHGNAYLENN 736  
 QY 519 -KISDLS-PLASLHQ-----LQELHIDNNQ--ITDLS PVSHKESLTVVDSL 560  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 737 YKVGEIKLPIPKLNQGTTTAGNKIPVTFMANAYLDNOSTYIVEV-PILEKENQT--- 790  
 QY 561 RNADV DLTQAPKLETLMVNNDTKVSHLDLKNNNP-LSSLSINRAQQLQSL--EGIEASS 617  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 791 -----DKPSILPOFKRNKAQENSKFDEKVEEPK 818  
 QY 618 VIVRVEAE-----GNOIKSLVLKD-----KQGSLTFLDV TG---NQLTSL EGVN NFT 661  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 819 TSEKVEKEKLSETGNSTSNTLEEVPTVDPVQEKVAFAESYGMKLENVLNFMDG--- 873  
 QY 662 ALDILSVSKNQLTNVL SKPNKTVTNIDISHNNISLADLKLNEOHIP EAIAKNFPAVY EG 721  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 874 -----TIELYLPGEV---IKKN---MADF---TGEA POGNGENKPS--EN 908  
 QY 722 SMVGN GTAEEKAAMATKAKESAQEA 746  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 909 GKVSTGTVENQPT-ENKPADSLPEA 932  
 RESULT 12  
 US-09-471-255-2  
 Sequence 2, Application US/09471255  
 GENERAL INFORMATION:  
 APPLICANT: BIOCHEM PHARMA INC.  
 APPLICANT: HAMEL, Jos,<sup>e</sup>  
 APPLICANT: BRODEUR, Bernard R.  
 APPLICANT: PINEAU, Isabelle  
 APPLICANT: MARTIN, Denis  
 APPLICANT: RIOUX, Cl'ment  
 TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
 FILE REFERENCE: 12806-11PCT  
 CURRENT APPLICATION NUMBER: US/09/471, 255  
 CURRENT FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: US 60/113, 800  
 PRIOR FILING DATE: 1998-12-23  
 NUMBER OF SEQ ID NOS: 102  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 LENGTH: 1039  
 ; TYPE: PRT  
 ; ORGANISM: S. pneumoniae  
 ; US-09-471-255-2  
 RESULT 13  
 US-09-583-110-5226  
 Sequence 5226, Application US/09583110  
 GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al.  
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
 ; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 5226  
; LENGTH: 1039  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae

Query Match 7.2%; Score 292.5; DB 19; Length 1039;  
Best Local Similarity 21.4%; Pred. No. 8e-13;  
Matches 185; Conservative 114; Mismatches 283; Indels 283; Gaps 45;

Qy 16 SQLTLIACQSRRGNGTYPITKOSRKGMTSNKIKPIKKSKTKNKTTHKGVAGVDFPT---- 70  
Db 237 SQLSYSSTASDNN-----TQSVAKGSTS--KPANKSENLQSLIKE--YDSPAQRYS 285  
Qy 71 -DDGFILTKDSKILSKTDQGIVVVDHDGHSHFIFYADLKG--SPFEYLIP--KGASL-- 121  
Db 286 ESDGLVF-DPAKILSRTTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 344  
Qy 122 AKP-----AVAQRAASQGTSK-VADPHHHEFNPADIVAEDALGYTVRHHDDHFHYIL 172  
Db 345 AKPNEVSSLGSLSSNPSSLTTSKELSSADGYIFNPKDIVEETATAYIVRHGDHFHYIP 404  
Qy 173 KSSLSGOTQAQAKOVATRLPQOTSSLVSTATANGIPGLHFPTSDGFOFNQGQIVGVTKDSI 232  
Db 405 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH---EKHEEDGYGFDANRTIAEDESGF 457  
Qy 233 LVDHDGHHLPISEADLROQQGWAHVADQYDPAKKAEPKAETHQT----- 275  
Db 458 VMSHGDNHYFFKKDLTE-----EQIKAQKHLEEVKTSHNGLDSLSSHEQDYPG 507  
Qy 276 --PELSEREKEYOKEKLAELKGIDPSTIKRVETQDGKLGLEYPHHDHAHVMLSDIEI 333  
Db 508 NAKEMKDLKKIEEKLAGIMKOQYGVKRESI--VVNKEKNALIYPHGDH----- 553  
Qy 334 GKDIIDPHATEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPPSNE---KD 388  
Db 554 -----HHADPIDEHKPVG-----TGHSHSNVELFKPEEGVAKKE 587  
Qy 389 PNMM--KEWLAVIKLDLGSRKDPLQRKGQLSLPNLETIGIFTPIKDISPVLFQKKLKQ 446  
Db 588 GNKVYTGEELTNVNL--LKNSTFNNQNFTLANGQKRVSFSPPELE-----KKLGI 637  
Qy 447 LLMKTGTVTDYRFID-----NMPOLEG---IDISONNLKDISFLS 483  
Db 638 NMLVKLITPDGKVLEKVGKVFEGVGNIANFIELDQPYLPQGOTFKYTIASKDYPEVSYDG 697  
Qy 484 KYKNLTLVA-----AADNGIEDIRPLQLP-NLKFLV-----LSNN 518  
Db 698 TFTVPTSLAYKMASQTFYPFHAGDTYL-VNPQFAVPKGTDALVRVDEFHGNAYLENN 756  
Qy 519 -KISDLS-PLASLHQ-----LQELHIDNQ-ITDLSPVSHKESLTWVDSL 560  
Db 757 YKVEGEIKLPIPKLNQGTTTAGNKIPVTMANAYLDQSTYIVEV-PILEKENOT--- 810  
Qy 561 RNADVDLATLQAPKLETLMVNNTDKVSHLDFLKNNP-LSSLSINRAQLOSL-EGIEASS 617  
Db 811 -----DKPSILPQFKRNKAQENSKLDEKEVEPK 838  
Qy 618 VIVRVEAE-----GNQIKSLVLUKD-----KQGSILTFLDVTG---NQLTSLLEGVNFT 661  
Db 839 TSEKVEKEKLSETGNSTSNSNLEEVPTVDPVQEKVAKFAESYGMKLENVLNFMDG---- 893

RESULT 14  
US-09-471-255-78  
Sequence 78, Application US/09471255  
GENERAL INFORMATION:  
APPLICANT: BIOCHEM PHARMA INC.  
APPLICANT: HAMEL, Jos, e  
APPLICANT: BRODEUR, Bernard R.  
APPLICANT: PINEAU, Isabelle  
APPLICANT: MARTIN, Denis  
APPLICANT: RIOUX, Cl,ment  
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 12806-11PCT  
CURRENT APPLICATION NUMBER: US/09/471,255  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/113,800  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 78  
LENGTH: 780  
TYPE: PRT  
ORGANISM: S. pneumoniae

Query Match 7.0%; Score 287; DB 18; Length 780;  
Best Local Similarity 25.6%; Pred. No. 1.3e-12;  
Matches 123; Conservative 63; Mismatches 166; Indels 128; Gaps 23;

Qy 16 SQLTLIACQSRRGNGTYPITKOSRKGMTSNKIKPIKKSKTKNKTTHKGVAGVDFPT---- 70  
Db 217 SQLSYSSTASDNN-----TQSVAKGSTS--KPANKSENLQSLIKE--YDSPAQRYS 265  
Qy 71 -DDGFILTKDSKILSKTDQGIVVVDHDGHSHFIFYADLKG--SPFEYLIP--KGASL-- 121  
Db 266 ESDGLVF-DPAKILSRTTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 324  
Qy 122 AKP-----AVAQRAASQGTSK-VADPHHHEFNPADIVAEDALGYTVRHHDDHFHYIL 172  
Db 325 AKPNEVSSLGSLSSNPSSLTTSKELSSADGYIFNPKDIVEETATAYIVRHGDHFHYIP 384  
Qy 173 KSSLSGOTQAQAKOVATRLPQOTSSLVSTATANGIPGLHFPTSDGFOFNQGQIVGVTKDSI 232  
Db 385 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH---EKHEEDGYGFDANRTIAEDESGF 437  
Qy 233 LVDHDGHHLPISEADLROQQGWAHVADQYDPAKKAEPKAETHQT----- 275  
Db 438 VMSHGDNHYFFKKDLTE-----EQIKAQKHLEEVKTSHNGLDSLSSHEQDYPG 487  
Qy 276 --PELSEREKEYOKEKLAELKGIDPSTIKRVETQDGKLGLEYPHHDHAHVMLSDIEI 333  
Db 488 NAKEMKDLKKIEEKLAGIMKOQYGVKRESI--VVNKEKNALIYPHGDH----- 533  
Qy 334 GKDIIDPHATEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPPSNE---KD 388  
Db 534 -----HHADPIDEHKPVG-----TGHSHSNVELFKPEEGVAKKE 567  
Qy 389 PNMM--KEWLAVIKLDLGSR-----KDPLORKGLSLPNLE-TLIGIFTPIKDISP 437  
Db 568 GNKVYTGEELTNVNLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINML-VKLITP 626

Mon Dec 3 01:34:19 2001

Sequence 56, Application US/09471255  
GENERAL INFORMATION:  
APPLICANT: BIOCHEM PHARMA INC.  
APPLICANT: HAMEL, Jos, e  
APPLICANT: BRODEUR, Bernard R.  
APPLICANT: PINEAU, Isabelle  
APPLICANT: MARTIN, Denis  
APPLICANT: RIoux, Cl'ment  
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 12806-11PCT  
CURRENT APPLICATION NUMBER: US/09/471, 255  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/113, 800  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 56  
LENGTH: 489  
TYPE: PRT  
ORGANISM: S. pneumoniae

Search completed: December 3, 2001, 07:22:27  
Job time: 516 sec

GenCore version 4.5  
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**OM protein - protein search, using sw model**

**Run on:** December 3, 2001, 07:16:08 ; Search time 39.47 Seconds  
(without alignments)  
**468.652 Million cell updates/sec**

**Title:** US-09-645-835A-6  
**Perfect score:** 4363  
**Sequence:** 1 VKKTYGGIGSVAAILLATHI.....YNKNGELVTYDIKTLOQINP 822

**Scoring table:** BLOSUM62  
Gapop 10.0 , Gapext 0.5

**Searched:** 212252 seqs, 22503292 residues

**Total number of hits satisfying chosen parameters:** 212252

**Minimum DB seq length:** 0  
**Maximum DB seq length:** 200000000

**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

- 1: Issued\_Patents\_AA:\*
- 2: /cggn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
- 3: /cggn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 4: /cggn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 5: /cggn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cggn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	1021.5	23.4	763	4 US-08-961-083-66
2	934	21.4	796	4 US-08-961-083-56
3	839.5	19.2	447	4 US-08-961-083-182
4	150.5	3.4	1588	5 PCT-US93-07261-11
5	150.5	3.4	1663	5 PCT-US93-07261-16
6	135.5	3.1	2465	2 US-08-596-291-3
7	135.5	3.1	2465	3 US-09-100-804-3
8	133	3.0	1541	4 US-08-296-791-3
9	133	3.0	1541	5 PCT-US95-10661A-3
10	131.5	3.0	1861	2 US-08-790-912-4
11	130.5	3.0	1848	4 US-08-296-791-6
12	130.5	3.0	1848	5 PCT-US95-10661A-6
13	130	3.0	765	2 US-08-663-112-2
14	129	3.0	1181	2 US-08-488-940-2
15	127.5	2.9	783	6 5231168-2
16	127.5	2.9	2466	3 US-09-080-855-12
17	127.5	2.9	2466	5 PCT-US94-09943-2
18	126.5	2.9	1194	2 US-08-488-940-1
19	126.5	2.9	2485	4 US-09-290-640-46
20	2.9	506	3 US-09-032-365A-19	
21	2.9	747	1 US-07-854-596B-40	
22	2.8	608	2 US-08-405-496A-21	
23	2.8	608	2 US-08-405-496A-21	
24	2.8	608	4 US-08-915-136-21	
25	2.8	609	1 US-08-480-604A-30	
26	2.8	609	4 US-08-915-136-30	
27	2.8	2366	1 US-08-480-604A-10	

**ALIGNMENTS**

RESULT	1
US-08-961-083-66	; Sequence 66, Application US/08961083
	; Patent No. 6159469
	<b>GENERAL INFORMATION:</b>
	APPLICANT: Choi et. al.
	TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
	NUMBER OF SEQUENCES: 452
	CORRESPONDENCE ADDRESS:
	ADDRESSEE: Human Genome Sciences, Inc.
	STREET: 9410 Key West Avenue
	CITY: Rockville
	STATE: Maryland
	COUNTRY: USA
	ZIP: 20850
	<b>COMPUTER READABLE FORM:</b>
	MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
	COMPUTER: HP Vectra 486/33
	OPERATING SYSTEM: MSDOS version 6.2
	SOFTWARE: ASCII Text
	<b>CURRENT APPLICATION DATA:</b>
	APPLICATION NUMBER: US/08/961,083
	FILING DATE:
	CLASSIFICATION: 435
	PRIOR APPLICATION DATA:
	APPLICATION NUMBER:
	FILING DATE:
	ATTORNEY/AGENT INFORMATION:
	NAME: Brookes, A. Anders
	REGISTRATION NUMBER: 36,373
	REFERENCE/DOCKET NUMBER: PB340P2
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: (301) 309-8504
	TELEFAX: (301) 309-8512
	INFORMATION FOR SEQ ID NO: 66:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 763 amino acids
	TYPE: amino acid
	STRANDEDNESS: single
	TOPOLOGY: linear
	MOLECULE TYPE: protein
	US-08-961-083-66

**Query Match** 23.4%; Score 1021.5; DB 4; Length 763;  
Best Local Similarity 32.9%; Pred. No. 1.6e-76;  
Matches 282; Conservative 101; Mismatches 238; Indels 237; Gaps. 32;  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 30, Appl  
Sequence 30, Appl  
Sequence 10, Appl

QY 22 SYOLGKHHMGLATKD-NQIAVIDDSSKGKVAKPTNKTMQDQISAEQIVVKITDQG 80

ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 796 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Qy 468 VKAKGQADELVAALDQEKGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDVFYARYOLDL 527  
Db 573 TKEKG---ILPPSPDADVKA  
PNTGDSAAA-----TYNR---- 602

Qy 528 TQIAFAEQELMLKDKKKHYRDIWDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHDH 587  
Db 603 -----VKGEKR-----IPLVRUPLPYMEHTVEVKGNLIPHDKH 636

Qy 588 IHVVVPYSWL-----TRNQIATIKYVMQHPEVRP---DVWSKPGHEESGSV  
VIPN 632  
Db 637 YHNIKFAWFDDHTYKAPNGTYLEDLFATIKYVEHHPDPERPHSNDGW-----GNASEH 688

Qy 633 VTPLDKRAGMPNNQTIHSAAEWO  
KALAEGRFAAPDGYIFDPRDVLAKETFWKDGFSFIP 692  
Db 689 VLGKKDHSEDPNKNAEDEEPV  
PEETPAE-----WP 720

Qy 693 RADGSSLRTINKSDLSQAEWOOAQELLAKKN---AGDATDT-----DKPEE 735  
Db 721 QVE-----TEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTIQIMDNNSI 771

Qy 736 KQQADK---SNENQOPSEASKEE 755  
Db 772 MAEAEKLALLKGNSNPSSVSKEK 794

RESULT 3

; Sequence 182, Application US/08961083

; Patent No. 6159469

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961, 083

PRIOR APPLICATION DATA:

FILING DATE: CLASSIFICATION: 435  
FILED DATE: FILING DATE: 4

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36, 373  
REFERENCE/DOCKET NUMBER: PB340P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 182:

SEQUENCE CHARACTERISTICS:  
LENGTH: 447 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-961-083-182

Query Match 19.2%; Score 839.5; DB 4; Length 447;  
Best Local Similarity 40.7%; Pred. No. 1e-61; Mismatches 119; Indels 85; Gaps 10;

---

Qy 29 HMLGLATKD-NQIAVIDD  
SKGVKAPKTNKTMDQISAE  
GISAEGISAEQIVW  
KITDQGYV  
TSHGD 87  
Db 4 HRSQENKD  
NNRVSYV  
DGSQS  
KS--ENLTPD  
QVSKEGI  
QAEQIV  
KITDQGYV  
TSHGD 61

Qy 88 HYHFYNGK  
VYPYDAL  
FSEELL  
MKDPN  
YQLK  
DADIV  
NEVKG  
GGYII  
KVDG  
KYYV  
LKA  
HAD 147  
Db 62 HYHYNGK  
VYPYDAL  
FSEELL  
MKDPN  
YQLK  
DADIV  
NEVKG  
GGYII  
KVDG  
KYYV  
LKA  
HAD 636

Qy 148 NIRT  
KQQIA  
EQVAK  
GTKE  
AKGLA  
QVHLS  
KEEV  
AAV  
NEAK  
RQGR  
YTT  
DDGY  
IF  
SPTDI 207  
Db 122 NVRT  
KDEIN  
RQK  
OEH  
VHKD  
-NE  
KV  
NS  
NV  
A-----  
VAR  
SQR  
GRT  
TND  
GYV  
FP  
ADI 169

Qy 208 IDDLG  
DAYLV  
PHGN  
HYT  
PK  
KDL  
SP  
SEL  
AAQ  
AWS  
SQ  
QGR  
GAR  
PS--  
DYR  
RPT  
PAP  
GRR 265  
Db 170 IEDTG  
NAYIV  
PHGG  
HYV  
IPK  
SDL  
SA  
ELAA  
KAHLA  
--  
GKN  
MQ  
PS  
SI  
SYS  
STAS  
DNNT 226

Qy 266 KAPI  
PDV  
TPN  
PGHQ  
P  
DNG  
GYH  
P  
APP  
RN  
P  
NDA  
S  
QN  
KH  
Q  
RDEF  
KG  
KT  
KEL  
L  
D  
L  
DK  
PSA 325  
Db 227 QSV  
AKGST  
SKP  
AN-----  
KSEN  
LQSL  
LKL  
EYL  
D  
PSA 257

Qy 326 YRH  
VEED  
GLT  
FEPT  
QV  
KS  
NA  
FGY  
VV  
PHGD  
HYH  
I  
TPR  
SQL  
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PLE  
M  
ADR  
Y  
LAG  
QT  
DD  
ND 385  
Db 258 QRY  
SES  
SDG  
LWF  
DP  
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STV 317

Qy 386 S-----  
GSDHS  
KPS--  
-DKE  
VHT  
FLG  
HRI  
KAY  
GKG  
LGD  
KP  
Y  
DTS  
DAY  
VFSK 429  
Db 318 STNA  
KPN  
EV  
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P 357

Qy 430 ESI  
HSV  
DKSG  
VTAK  
HGD  
HF  
HYI 451  
Db 358 KDI  
VEET  
ATA  
YIV  
R  
HGD  
HF  
HYI 379

RESULT 4

PCT-US93-07261-11

; Sequence 11, Application PC/TUS9307261

GENERAL INFORMATION:

TITLE OF INVENTION: PFEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: John H. C. Blasdale  
STREET: One Giralta Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940-1000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.5  
SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07261

FILING DATE: 19930805

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927, 531

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.  
REGISTRATION NUMBER: 31, 895  
REFERENCE/DOCKET NUMBER: DX0288K

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7398  
TELEFAX: 201-822-7039

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1588 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
MOLECULE TYPE: protein

PCT-US93-07261-11

Query Match 3.4%; Score 150.5; DB 5; Length 1588;  
 Best Local Similarity 19.7%; Pred. No. 0.0019; Mismatches 364; Indels 243; Gaps 40;  
 Matches 183; Conservative 137; Mismatches 364; Indels 243; Gaps 40;

Qy 34 TKDNQIAYIDDSKGKVAKPTN-----KTMDOQISAEEGISAEQIVKITDQGYVTSHGDH 88  
 |: |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 11 TEKNEKARNALKEKKLKEQKKNDQAQAKDLTJKESODSSEKSILKEVNGEALKEKE-- 67  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 89 YHFYNGKVPYDAIISEELLMTDPNYHKQSDVINEILDG--YVIKVNGN---YYVYLK 141  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 68 -----NKETLKKKELENQKEKEENKNKIKDNNDDEALKNKGNDDKKIVPKK 113  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 142 PGSKRKNIR-----TKQQIAEQVAKGTKEAKER-----GLAQVAHLSKEEV 182  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 114 PESVEKDLKEMELKEKEFIQKHLKDYEERKEERKRNWLRSLLRKREIEOLEKLNAQE 173  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 183 AVNEAK-----ROGRYTDDGYIFSPTD-----IIDDLGDAY--L 216  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 174 SAINELKERRASRRPMMVKMQRGMKDEVDEWIKKYDDEQAENGTKEEEIKDKGDGYEEI 233  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 217 VP---HGNHYHYIPKKDLSPSELAAQAYWSQOKGRGARPSDYRPTPAPG---RRKAPIP 270  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 234 VETKFYGMRENALGELD-EYEERYEKRYYLKEDGEGLDKDVEEKLEETGYGFREKFPT 292  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 331 EDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPIRSQLSPLEMELADRYLAGQTDDNSGSD 389  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 332 SDDKVVVPVNKNKSSFPDKFRAPDKKRTMFYRLSELFPI-VPRKDNELAvgdsm--- 386  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 390 HSKPSDKEVTHF-----LGHRIKAYGKGL-----DGKPYDT 421  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 387 -SKVNGKKLKSTFNPFKRRNLKERKMQELHKFKKNYKQKLLEREKRENPDGEPLNT 445  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 422 SDAYVFSKESIHSSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVK----- 469  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 446 PEIHWIRPSDL--MDK-GENKSAGHGPFKYQOPTKGLKEYEESHVSKDYQLEHEPTKLPEY 502  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 470 AKGQADELVAALDQEOGKEKPLFDTKVKSRKVTKDGKVGYIMPKDGKDYFVARYQLD--- 526  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 503 EKGHVSR-EYQOLDHEPPTKLPEYEGHVSRREYQOLDNEG 561  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 527 -LTQIAFAEQEML-KDKKHYRYDIVDTGIEPRLA--VDVSSLPMHAGNATYDTGSSFVI 582  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 562 PSTLKEYDQTELAKGKDITNKP-HESVDEYD----- 613  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 583 PHIDHIVWPYSWLTRNQIATIKYVMQHPEVRPD-----VWSKPGHEESGSI 630  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 614 -----QSELAKGKDITNKPRESVEDQTELAKGKEVTNKP-HENLEY- 656  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 631 PNVTPLDRKAGMPNWQOIHSAAEVOKALEGR----FAAPDGYIFDPDVLAKEFW 684  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 657 -NETDLAKGKEVTNKPRESVEDYDOSELAKGKDITNKP-HESVDEY--DCTELAK---- 707  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 685 KGDSFSIPRADGSSLRTINKSDLSQAEWOOAQELL--AKKNAGDATDTKPEEKQADKS 742  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 708 ---GKEVTNARENLEEEYNETDLA----KGKEVTNARENLEEEYNETDLA 759  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 743 NENOQ---PSEASKEESEDDFIDSPLPDYGLDRATELDHINQLAQKANIDPKYLIFQPEG 799  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 760 HENLEEEYNETDLAKGKEVTNKAHENLEEY-----NETDLAKGKEVTNKA 806  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 800 VQFYNN---KNGELVWTYDITLQOIN 821  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 807 LEEYNETDLAKGKEVTNARENLEEEY 833  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 RESULT 5  
 PCT-US93-07261-16  
 Sequence 16, Application PC/TUS9307261

GENERAL INFORMATION:  
 TITLE OF INVENTION: PFEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John H. C. Blasdale  
 STREET: One Giralta Farms  
 CITY: Madison  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07940-1000  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.5  
 SOFTWARE: Microsoft Word 5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/07261  
 FILING DATE: 19930805  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/927,531  
 FILING DATE: 07-AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Blasdale, John H. C.  
 REGISTRATION NUMBER: 31,895  
 REFERENCE/DOCKET NUMBER: DX0288K  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-822-7398  
 TELEFAX: 201-822-7039  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1663 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Plasmodium falciparum  
 STRAIN: Malayan Camp  
 PCT-US93-07261-16

Query Match 3.4%; Score 150.5; DB 5; Length 1663;  
 Best Local Similarity 19.7%; Pred. No. 0.002; Mismatches 364; Indels 243; Gaps 40;  
 Matches 183; Conservative 137; Mismatches 364; Indels 243; Gaps 40;

Qy 34 TKDNQIAYIDDSKGKVAKPTN-----KTMDOQISAEEGISAEQIVKITDQGYVTSHGDH 88  
 |: |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 11 TEKNEKARNALKEKKLKEQKKNDQAQAKDLTJKESODSSEKSILKEVNGEALKEKE-- 67  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 89 YHFYNGKVPYDAIISEELLMTDPNYHKQSDVINEILDG--YVIKVNGN---YYVYLK 141  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 68 -----NKETLKKKELENQKEKEENKNKIKDNNDDEALKNKGNDDKKIVPKK 113  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 142 PGSKRKNIR-----TKQQIAEQVAKGTKEAKER-----GLAQVAHLSKEEV 182  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 114 PESVEKDLKEMELKEKEFIQKHLKDYEERKEERKRNWLRSLLRKREIEOLEKLNAQE 173  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 183 AVNEAK-----ROGRYTDDGYIFSPTD-----IIDDLGDAY--L 216  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 174 SAINELKERRASRRPMMVKMQRGMKDEVDEWIKKYDDEQAENGTKEEEIKDKGDGYEEI 233  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 217 VP---HGNHYHYIPKKDLSPSELAAQAYWSQOKGRGARPSDYRPTPAPG---RRKAPIP 270  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 234 VETKFYGMRENALGELD-EYEERYEKRYYLKEDGEGLDKDVEEKLEETGYGFREKFPT 292  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 331 EDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPIRSQLSPLEMELADRYLAGQTDDNSGSD 389  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Db 332 SDDKVVVPVNKNKSSFPDKFRAPDKKRTMFYRLSELFPI-VPRKDNELAvgdsm--- 386  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |  
 Qy 390 HSKPSDKEVTHF-----LGHRIKAYGKGL-----DGKPYDT 421  
 |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: | : |: |

Db 387 -SKVNGKKLKSTFNPFKRRRNKLKERKMQELHKFKKNYQKLLEREKRENPDGEPLNT 445  
 Qy 422 SDAYVFSKESIHSVSDKSGVTAKHGDHFHYIGFGELEQEYELDEVANWVK----- 469  
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 446 PETHVTRPSDL--MDK-GENKSAGHPEKYQPTKGLKEYEESHSVSKDYQLEHEPPTKLPEY 502  
 Qy 470 AKGQADELVAALDQEQQKEKPLFDTKVSRKVTKDGKVGYIMPDKDGFYARYQLD-- 526  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 503 EKGHVSR-EYOLDHEPPTKLPEYEKGHVSREYQLDNEG 561  
 Qy 527 -LTQIAFAEQEML-KDKKHRYDIVDTGIEPRLA--VDVSSLPMHAGNATYDTGSSFVI 582  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 562 PSTLKEYDQTELAKGKDITNKPHESVDEYDQTELAKGKDITNKPHESVDEYD-- 613  
 Qy 583 PHIDHIIHVVPYSWLTRNOIATIKYVMQHPEVRPD-----VNSKGHEESGVI 630  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 614 -----QSELAKGKDITNKPHESVDEYDQTELAKGKDITNKPHESVDEYD-- 656  
 Qy 631 PNVTPLDKRAGMPNWOIHSAAEVQKALAEGR-----FAAPDGYIFDPDRDVLAKEFVW 684  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 657 -NETDLAKGKEVTKARENLEEEYNETDLA---KGKEVTKARENLEEEYNETDLA--- 707  
 Qy 685 KDGFSFISPRADGSSLRTINKSDLSQAEWQQAELL--AKKNAGDATDTDKPEEKQADKS 742  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 708 --GKEVTKARENLEEEYNETDLA---KGKEVTKARENLEEEYNETDLA--- 759  
 Qy 743 NENQQ---SEASKEEKESDDFTDSLPGYGLDRATLEDHINQLAQKANIDPKYLIFQPEG 799  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 760 HENLEEEYNETDLAKGKEVTKAHENLEEY-----NETDLAKGKEVTK---AHEN 806  
 Qy 800 VQFYN-----KNGELVTDIKTLQQTN 821  
 ; | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 807 LEYNETDLAKGKEVTKARENLEEEY 833

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RESULT 6  
 US-08-596-291-3  
 Sequence 3, Application US/08596291  
 ; Patent No. 5821075  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GONEZ, LEONEL JORGE  
 ; APPLICANT: SARAS, JAN  
 ; APPLICANT: CLAESON-WELSH, LENA  
 ; APPLICANT: HELDIN, CARL-HENRIK  
 ; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
 ; NUMBER OF SEQUENCES: 4  
 ; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
 ; STREET: 600 ATLANTIC AVENUE  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: USA  
 ; ZIP: 02210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/596, 291  
 FILING DATE: 09-AUG-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/115, 573  
 FILING DATE: 01-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GATES, EDWARD R.  
 REGISTRATION NUMBER: 31, 616  
 REFERENCE/DOCKET NUMBER: LO461/7000  
 TELECOMMUNICATION INFORMATION:

Query Match 3.1%; Score 135.5; DB 2; Length 2465;  
 Best Local Similarity 19.6%; Pred. No. 0.067;  
 Matches 172; Conservative 114; Mismatches 328; Indels 265; Gaps 4  
 Query 9 GSVAAILLATHIGSYQLGKHHMGL---ATKDNQIAVYIDDSSKGKVAPKTNKTM-QISAE 64  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1422 GQWHLLEK--GQSPSTSKEHVVPVTQOCTLSDONA--QGQPEVKTTQVKDYSFVTE 1476  
 Query 65 EGISEAQIVVVKITDQGYVTSQGDHYHFYNGKPYDATIISEELLMTPNYHFQSDVINEI 124  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1535 L----KVNG---ASLKGLSQOEVISALRTAPEVFLLCRPPPGVLFELDTALLTFLQS 1586  
 Query 125 LDGYVIVKVNQNYVVLKPGSKRKNIIT-----KQQ 154  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1587 PAQVLPNSSKDSQSPSCVEOSTSSDENEMSDSKKOCKSPSRRDSYSDSSGSGEDDLVTA 1646  
 Query 204 PTDIIDDLGDAYL-----VPHGNHYH1PKKDLSPSELAAQAYWSQOKRGARPSDY 256  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1647 PANINSTWSSALHOTLSNMVSQAOQSHHEAPK---SOEDTICTMFYVYPOKIPNKPEEFD 1703

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Query 257 RPTPAPGRRKAPIPDVTNNPGQGHQPDNGGYHPAPPNDASQNKHQRDEFKGKTFKELL 316  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1704 NPSPLP-----PDMA--PGQSYQPOS-----ESASSSSMDKYHIIHISEPTROENW 1747  
 Query 317 DQLHRLDKYRVEEDGLIFE-PTQVIKSNAFGYVVPHDHYH1IPRSQSLPLEMELA 373  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1748 TPL-KNDLE-NHLEDFELEVELLITLIKSEKASLGFTVTKGN-----QRI 1790  
 Query 374 DRYLAGTDDNDSGSDHSKPSDKEVTHFLGRHIKAGKGLDGKPYDTS DAYVFSKESIH 433  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1791 GCYVHVDVIQDPAKSDGRIKPGDRLI-----KVN 1818

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Query 434 SVDKSGVTAKHGDHFHYIGFGELEQEYELDEVANWVKAGQADELVAALDQEQQKEKPLFD 493  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1819 DTDVNTM-----HTD-----AVNLLRAASKTVRLV-----GRVPRITO 1853  
 Query 494 TKVSRKVT-KDGKVGYIMPKDGKDFYARYQLDLT-QIAFAEQEMLKDKHY 545  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1854 NTNVASFATGKHLTCNKEELGFSLCGGHDLSLYQWVYISDINPRSAIAEGNLQLLDVH 1913

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Query 546 RYDIVDTGI---EPRLAVIDVSSLPMHAGNATYDTGSSFVIPHIDHIIHVVPYSWLTRNQIA 602  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1914 VNGVSTQGMTEEVNRLADM-SLP-----SLVLK-----ATRNDLP 1948  
 Query 603 TIKYMQHPEVRPDVWSKGHEESGVT-PNVTPLDKRAGMPNWOIHSAAEVQKALAEQ 661  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1949 VWPSSKRSAVSPKSTKGNGSYVGSCSQPALTPNDSFSTV-----AGEEINE---- 1996  
 Query 662 RFAAPDGYIF----DPRDVLAKEFWVKDGFSI PRADGSSLRTINKSDLSQAEWQQA 715  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1997 -ISYPKGKCSTYQIKGSPNLTLPKESYIQEDDIY----DDSQEAEVIOSSLWD-EEA 2049  
 Query 716 QELLAKKN-AGDA-----TDTD---KPEEKQQADKSN-----ENQ 746  
 ; | :| ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 2050 ONLNENNAAGDSCGPGLTLKMNGKLSEERTEDDCDGSPPLPEYFTEATKMGCEYCEEK 2109  
 Query 747 QPSEA----SKEEKESDDFI----DSLPGYGLDRATLED 777

Db 2110 VKSESLIQQPKQEKKTDDDEITWGNDLPL---IERTNHED 2145  
 RESULT 7  
 US-09-100-804-3  
 ; Sequence 3, Application US/09100804  
 ; Patent No. 6066472  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GONEZ, LEONEL JORGE  
 ; APPLICANT: SARAS, JAN  
 ; APPLICANT: CLAESSEN-WELSH, LENA  
 ; APPLICANT: HELDIN, CARL-HENRIK  
 TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
 TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
 TITLE OF INVENTION: TYROSINE PHOSPHATASES  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
 STREET: 600 ATLANTIC AVENUE  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/100, 804  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/596, 291  
 FILING DATE: 09-AUG-1996  
 APPLICATION NUMBER: US 08/115, 573  
 FILING DATE: 01-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GATES, EDWARD R.  
 REGISTRATION NUMBER: 31, 616  
 REFERENCE/DOCKET NUMBER: LO461/7003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-720-3500  
 TELEFAX: 617-720-2441  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2465 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-100-804-3

Query Match 3.1%; Score 135.5; DB 3; Length 2465;  
 Best Local Similarity 19.6%; Pred. No. 0.067;  
 Matches 172; Conservative 114; Mismatches 328; Indels 265; Gaps 44;

QY 9 GSVAAILLATHIGSQQLGKHHMGL---ATKDNOIAYIDDSKGKVAKPTNKTM-QISAE 64  
 Db 1422 GOVVLHLLEK--GQSPTSKEHVPVTPOCTLSQDNA--QGQGPEVKVKTQVKDYSFVTE 1476  
 QY 65 EGISAECIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELMTDPNYHKQSDVINEI 124  
 Db 1477 ENTFEVKLFKNSSGGLGFSFSRDL---NLIEQINASIVRKVLFAQPAAESGKIDVGDV 1534  
 QY 125 LDGYVIKVNGNYWYVLPGSKRKNIRT-----KQQ 154  
 Db 1535 L-----KVNG---ASIKGLSQQEVISALRGTAPEVFLLCRPPPGVLPEIDTALLTPIQS 1586

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QY 155 IAFQVAKGTKEAKEKGGLAQVAHLSEEVAANEAKE----ROGRYTT----DDGYIFS 203  
 Db 1587 PAQVLPNSSKDSQSPSCVEQSTS DENEMS KSKKQCKSPSRD SYSDSSGSGGEDDLVTA 1646  
 QY 204 PTDIIDDLGDAYL----VPHGNHYHYIPKKDLSPSELAAQAYWSQOKQGRGARPSDY 256  
 Db 1647 PANISNSTWSSALHOTLSNMVSQAQSHHEAPK--SQEDTICTMFYQPQKIPNKFEDS 1703  
 QY 257 RPTPAPGRKAPIPDWTNPNGQHQPDNGGYHPAPPN DASONKHKORDEFKGKTFKELL 316  
 Db 1704 NPSPSLP----PDMA--PGQSYQPOS----ESASSSSMDKYHHTHISEPTROQEW 1747  
 QY 317 DQLHRLDKYRHEEDGLIFE-PTQVIKSN--AFGYVPHGDHYHITPRSQLS PLEMELA 373  
 Db 1748 TPL-KNDLE -NHLEDFELEVELLITLIKSEKASLGFVTKGN-----QRI 1790  
 QY 374 DRYLAGQTDDNSGSDHSKPSDKEVHTFLGHRIKAYKGKLDGKPYDTS DAYVFSKETH 433  
 Db 1791 GCYVHDVIQDPAKSDGRLKPGDRLI-----KVN 1818  
 QY 434 SVDKSGVIAKHGDFHYYIGFGELEQYELDEVANWVKAGQADELVALDOEQKEKPLFD 493  
 Db 1819 DTDVTINMT--HTD-----AVNLLRAASKTVRLV-----GRVPRITO 1853  
 QY 494 TKKVS----RKVT-KDGKVGYIMPKDGDYFYARYQOLDLT--QIAFAEOELMLKDKHY 545  
 Db 1854 NTNIVASFATGHKLTCNEELGFSLCCGGHDSLQYVWYISDINPRSAVATEGNLQLLDVHY 1913  
 QY 546 RYDIVDTGTI---EPRLAUDVSSLPMHAGNATYDTGSSFWVPHIDHTHVWPYSWLTRNQIA 602  
 Db 1914 VNGVSTQGMTEEVNRALDM-SLP-----SLVLK-----ATRNDLP 1948  
 QY 603 TIKVWMQHPEVRPDVWWSKGPGHEEGSVT-PNVTPLDKRAGMPNWQI IHSAAEVQKALAEG 661  
 Db 1949 VVPSSKRSAVSAPKSTKGNGSYSVGSCSQPALTPNDSFSTV-----AGEEINE---- 1996  
 QY 662 RFAAPDGTYF-----DPRDVLAKETEVWKDGSEFISPRADGSSLRTINKSDLSQAEWQA 715  
 Db 1997 -ISYPKGKCSSTYQIKGSPNLTLPKESYIQEDDIY-----DDSQEAEVIOSLLDVD-EEA 2049  
 QY 716 QELLAKKN-AGDA-----TDTD---KPEEKQADKSN-----ENQ 746  
 Db 2050 QNLINNENNAAGDSCCGPGLKMNGKLSEERTEDTDCDGSPPLPEYFTEATKMN GCEEYCEEK 2109  
 QY 747 QPSEA---SKEEKESDDFI---DSLDPYGLDRATLED 777  
 Db 2110 VKSESLIQQPKQEKKTDDDEITWGNDLPL---IERTNHED 2145

RESULT 8  
 US-08-296-791-3  
 ; Sequence 3, Application US/08296791  
 ; Patent No. 6245337  
 ; GENERAL INFORMATION:  
 ; APPLICANT: St. Geme III, Joseph W.  
 ; APPLICANT: Falkow, Stanley  
 TITLE OF INVENTION: Haemophilus Adherence and Penetration  
 TITLE OF INVENTION: Protein  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296,791  
 FILING DATE: 25-AUG-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Trecartin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1541 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 US-08-296-791-3

Query Match 3.0%; Score 133; DB 4; Length 1541;  
 Best Local Similarity 18.0%; Pred. No. 0.051; Mismatches 305; Indels 292; Gaps 37;

Matches 155; Conservative 108; Mismatches 305; Indels 292; Gaps 37;

Db 44 DSKGVKA-PKTNKTMQDQISAEEGISAQIVVKITDQGYVTSHGDHYHFYNGK 95  
 Qy 96 ---VPYDAI-ISEELIMTDPN-YHKOSDVIN- 122  
 Db 522 LDLNGNSLTDFHNRNIDDGARLNVHNMNTNASNITITGESLITDPNTITPYNIDAPDEDNP 581  
 Qy 123 ---EILDG-YVIKVNGNYVVLKPGRKRNII-RTKQQIAEQVA 160  
 Db 582 YAFRRIKDGGQLYLNLENYYALRKASTRSELPKNSGESNEWLYMGKTSDEAKRNM 641  
 Qy 161 K-GTKEAKEKGGLAQVAHLSEEVAVNEAKROGRYTFDDGYIFSPTD 206  
 Db 642 NHINNERMNGFNGYFGEEEGKNNGNLNVTFKGKSE-ONRFLLTGG-TN 687  
 Qy 207 I TIDL-----GDAYL-----VPHGNHYHI-PKKD-LSPSELAAQAYWSQKQRGARPS 254  
 Db 688 LNGDLTVEKGTLFLSGRPTPHARDIAGISSTKKDPHFAENNEVWVVEDWINR- 739  
 Qy 255 DYRPTPAPGRKAPPIDPVTPNPGOHPDNGGYHPPRPNDAQNKHQ- 303  
 Db 740 ---NFKATTMNVT-GNASLYSGRNVNANITSNITASNAQVHIGYKTGDTV 785  
 Qy 304 --RDEFKGK-TKEELDOLRRLDKYRHEEDGLIFEPTQVI-KS 344  
 Db 786 CVRSVDYTGVTCTDKLSKALN-SFNPTNLRGNVNLTESANFVLGKA 832  
 Qy 345 NAFGYVVPHGD-HYHILIPRSQSLPELEMELADRYLAGOTDDNDGSDHSKPSD 395  
 Db 833 NLFGTIQSRGNSQWRLTENSHTWHLTGNSDH-QLDLANGHILNSADSN- 881  
 Qy 396 KEYTHTEFLGHRIKAYGKGLDGKPYDTSAYFSKESIHSVDKSGVTAKGHDHFHYIGFE 455  
 Db 882 -NVT---KYNTL---TVNLSLNGNC-SFYYL-TD 905  
 Qy 456 LEQYELDEVANWVKAKGQADELVAALDQEQQ-KEKPLFDTKVSRKVTKDGKVGYIMPKD 514  
 Db 906 LSNKQGDKVWTKSATGNTLQVADKTGEPNHNELTFLDASKAQRDHLNVSLVGNNTVLDG 965  
 Qy 515 GKDY-FYARYQOLDLQIAFAEQELMLKDKHHYRDIVDGTGIEPRLAVIDVSSLPMHAG 570  
 Db 966 AWKYKLNVNGRYDLYNPEV-EKRNOTVDTTNITPNNIQADVPSVP-- 1011  
 Qy 571 NATYDTGSSFVIPHIDHTHVVPPYSWLTRNQIATIKYVMQHPEVRPDVWSKPGHEESGVI 630  
 Db 1012 ---SNNEELARVDEAPVPPAP-PSETTEVAENSKQESKTE 1052  
 Qy 631 PNVTPLDKRAGMPNWQIHSAAEVQKALAEGRFAAPPGYTFDPRDVLAKETFVWKDGFS 690

Db 1053 KNEQDATEAQ-NREVAKEAKSNVKANTQTNEVAQSG-SETKETOTTET----- 1100  
 Qy 691 IPRADGSSLRTINKSDLSOAEMQAOELLAKKNAGDATDTDKPEEKQ-QADKSNE 744  
 Db 1101 -----KETATVEKEEKAVETEKTEKQEV----PKVTSQVSPQESETVOPQAEPARE 1148  
 Qy 745 NQQPSEASKEESESDDFIDS 764  
 Db 1149 NDPTVNIKEPQSQTNTTADT 1168

RESULT 9  
 PCT-US95-10661A-3  
 Sequence 3, Application PC/TUS9510661A  
 GENERAL INFORMATION:

APPLICANT: Washington University, et al.  
 TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein  
 NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/10661A  
 FILING DATE: 16-AUG-1995  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/296,791  
 FILING DATE: 25-AUG-1994  
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
 NAME: Trecartin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: A-59941/RFT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1541 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 PCT-US95-10661A-3

Query Match 3.0%; Score 133; DB 5; Length 1541;  
 Best Local Similarity 18.0%; Pred. No. 0.051; Mismatches 305; Indels 292; Gaps 37;

Matches 155; Conservative 108; Mismatches 305; Indels 292; Gaps 37;

Db 44 DSKGVKA-PKTNKTMQDQISAEEGISAQIVVKITDQGYVTSHGDHYHFYNGK 95  
 Db 462 DNKGSLKVGDGTWILKQQTNGSGQHAFASVGIVGSRSTLVNLDDKQVDPNSIYFGFRGGR 521  
 Qy 96 ---VPYDAI-ISEELIMTDPN-YHKOSDVIN- 122  
 Db 522 LDLNGNSLTDFHNRNIDDGARLNVHNMNTNASNITITGESLITDPNTITPYNIDAPDEDNP 581  
 Qy 123 ---EILDG-YVIKVNGNYVVLKPGRKRNII-RTKQQIAEQVA 160  
 Db 582 YAFRRIKDGGQLYLNLENYYALRKASTRSELPKNSGESNEWLYMGKTSDEAKRNM 641  
 Qy 161 K-GTKEAKEKGGLAQVAHLSEEVAVNEAKROGRYTFDDGYIFSPTD 206  
 Db 642 NHINNERMNGFNGYFGEEEGKNNGNLNVTFKGKSE-ONRFLLTGG-TN 687

APPLICATION NUMBER: US 60/026,939  
 FILING DATE: 23-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Leary, Kathryn  
 REGISTRATION NUMBER: 36,317  
 REFERENCE/DOCKET NUMBER: 7600-4U1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 567-2991  
 TELEX: 831-494  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1861 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-790-912-4

Query Match 3.0%; Score 131.5; DB 2; Length 1861;  
 Best Local Similarity 18.1%; Pred. No. 0.091;  
 Matches 180; Conservative 118; Mismatches 316; Indels 383; Gaps 45;

Query 97 PYDAILISEELMLMDPNYHFKQSDVINEILDGYVIKVN---GNYVVYL-KPGSKRNI 149  
 Db 245 PQDEVLSGR--VAKPELLYKETSIETEIAVGEQIQENPDLAEGTVRKQEGKPGRKIEW 302

Query 571 NATYDTGSSFWIPIHDHIHVVPYWSLWRNQIATIKYVMQHPEVRPDVWPKGPHEESGWT 630  
 Db 1012 -----SNNEEIAARVDEAVPVPAPAT-----PSETTETVAENSKQESKTE 1100

Query 631 PNVTPPLDKRAGMPNMQTIHSAEVQKALAEGRFAAPDGYIFDPDVLAKEFVWKDGFS 690  
 Db 1053 KNEQDATETTAQ-NREVAKEAKSNVKANTQTNEVAQSG--SETKETOTT----- 1148

Query 691 IPRADGSSLRTINKSLSQAEMQQAQELLAKKNAGDATTDKPEEKQ---QADKSNE 744  
 Db 1101 -----KETATVEKEEKAVETEKTOEV-----PKVTQSQVSPKQEQSETVQPQAEARE 1148

Query 745 NOQPSEASKEESEDDFFDS 764  
 Db 1149 NDPTVNIKEPQSONTTADT 1168

RESULT 10  
 US-08-790-912-4

Sequence 4, Application US/08790912  
 Patent No. 5976542

GENERAL INFORMATION:  
 APPLICANT: Weiser, Jeffrey N.

APPLICANT: Plaut, Andrew G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
 TITLE OF INVENTION: OF STREPTOCOCUS PNEUMONIAE INFECTION  
 NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19103-2398

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/790,912  
 FILING DATE: 29-JAN-1997  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:

QY 207 IIDDL---GDAYL---VPHGNHYHYI--PKKD--LSPSELAAQAYWSOKQGRGARPS 254  
 Db 688 LNGDLTVEKGTLFLSGRPTPHARDIAGISSTKKDPHFAENNEVVVEDDWINR----- 739

QY 255 DYRPTPAPGRRKAPIPDVTNPNGQGHOPDNGGYHPAPPRNDAQSQNKHQ----- 303  
 Db 740 -----NFKAATTMNVT----GNASLYSGRNVNANTSNTASNKAQVHIGYKTGDTV 785

QY 304 --RDEFKGK---TFKELLQDHRLKYRVEEDGLIFEPTQVI-----KS 344  
 Db 786 CVRSDTYGTGVCTTDKLSDKALN-----SFNPTNLGNVLTESANFVLGKA 832

QY 345 NAFGYVVPHGD-----HYHILPRSQLSPLLEMELADRYLAGQTDNDSDGSDHSKPSD 395  
 Db 833 NLFGTIIQSRGNSQWRLTENSHWHLTGNSDH--QLDLANGHILNSADNSN----- 881

QY 396 KEVTHTFLGHRKAYGKGLDGKPYDTSAYVFSKESIHSDVKGVTAKHGDHFHYIGFE 455  
 Db 882 -NVT-----KYNTL-----TVNLSLSGN-----SFYVL--TD 905

QY 456 LEQYELDEVANWVKAKGQADELVAALDQEQQ-KEKPLFDTKVSRKVTKDGKVGYIMPKD 514  
 Db 906 LSNKQGDKVWVTKSATGNFTLQVADKTGEPHNHNLTVLNVSLVGNNTVDLG 965

QY 515 GKDY---FYARYQOLDLTOQIAFAEQELMLDKKKHYRDIWDTGIEPRLAVDVSLLPMHAG 570  
 Db 966 AWKYKLRNNGRYDLYNPEV-----EKRNQTVDTTNITTPNNIQADVPSVP--- 1011

QY 571 NATYDTGSSFWIPIHDHIHVVPYWSLWRNQIATIKYVMQHPEVRPDVWPKGPHEESGWT 630  
 Db 1012 -----SNNEEIAARVDEAVPVPAPAT-----PSETTETVAENSKQESKTE 1100

QY 631 PNVTPPLDKRAGMPNMQTIHSAEVQKALAEGRFAAPDGYIFDPDVLAKEFVWKDGFS 690  
 Db 1053 KNEQDATETTAQ-NREVAKEAKSNVKANTQTNEVAQSG--SETKETOTT----- 1148

QY 180 -----TKQQIAEQVAKGTKEAKEKGL-----AQWAHLSK-- 179  
 Db 303 RIFTVDNAEVSVREVLISTKIEEATPKIVEKGKLEAPSEKPVTSNLVQPEQVAPLPEYTG 362

QY 180 -----EVAAVNEAKRQGRY-TDDGYIFSPTDIDDLG---DAYLVPHGNHYH 225  
 Db 363 VOSGATIVEPEQVQASLPE-----YSGTLSGAIVEPEQOPELPEIGGVQSGAIVEPE---QV 412

QY 226 IPKKD-----LSPSELAAAQAYWSOKQGRGARPSDYSRPTP-----APGRRK 266  
 Db 413 TPLPEYGTGTQAGAWVSPSEQVAPLPPEYGTQSGAIVEPAQVTPLPPEYGTQVQSGAIVVKPAQV 472

QY 267 APIPD-----VTPNP-----GOGHQPD-- 283  
 Db 473 TPLPEYGTGTQSGAIVEPEQVTPSPETYGTQVQAGAIVEPEQVQASLPEYGTGSQAGAIVEPEQV 532

QY 284 -----NGGYHPAPPNND---ASQNKHORDE-FKGKTFKELL-QLHRL-DLKRY-HV 329  
 Db 533 EPQOEYTGNIEPAAPEAENPTEKAQPKQPEKEPKNIELRNVSDVELYSLADGKYKOHV 592

QY 330 EEDGLIFEPTQVIKSNAFGYVVPHGDHYHILPRSQLSPLLEMELADRYLAGQTDNDSDGSD 389  
 Db 593 SLD-----AIPSNCENYFK-----VKSSEKFDFLPI-----SIVD 625

QY 390 HSKPSDKEVTHFLGHRKAYGKGLDGKPYDTSAYVFSKESIHSDVKGVTAKHGDHFH 449  
 Db 626 STK-----DGQPVYKITA---SAEKL---KODVNNKYEDNFT 656

QY 450 YIGFGELEQYELDEVANWVKAKGQADELVAALDQEQQGKEKPLFDTKVSRKVTKDGKVGY 509  
 Db 657 FYLAKKAER---EVTNFT----SFSNLVQAINNLLNGTYLAASLNAVELENGASSY 708

QY 510 YM-----PKDGKDFYARYQOLDL---TOIAFAEOELMLDKKKHYRDIWDTGIEP 556  
 Db 709 IKGRFTGKLFGSKDGN--YAIYNKKPLFDTLSAATVENLTLKD-----VNI 754

QY 557 RLAVDVSLLPMHAGNATYDTGSSFWIPIHDHIHV----- 590  
 Db 755 SGKTDIGALANEANNAT-----RINNVHVDVLAGERGIGGLVWKA DNSKISNS 804

QY 591 -----VPY-----SWLTRNQIATIKYVMQHPEVRPDVWPKGPHEES 626  
 Db 805 FKGRIVNSYETKAPYNIGGLVQQLTGINALVUDSKATITISSNADSTNOTVGGLAGLVEK 864

QY 627 GSVIP-----NVTPLDKRAGMPN-WQ----- 646

RESULT 11  
 US-08-296-791-6  
 Sequence 6, Application US/08296791  
 Patent No. 6245337  
 GENERAL INFORMATION:  
 APPLICANT: St. Geme III, Joseph W.  
 APPLICANT: Falkow, Stanley  
 TITLE OF INVENTION: Haemophilus Adherence and Penetration  
 TITLE OF INVENTION: Protein  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/296,791  
 FILING DATE: 25-AUG-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Trecartin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1848 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 US-08-296-791-6

---

RESULT 12  
 PCT-US95-10661A-6  
 Sequence 6, Application PC/TUS9510661A  
 GENERAL INFORMATION:  
 APPLICANT: Washington University, et al.  
 TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:

Query Match 3.0%; Score 130.5; DB 4; Length 1848;  
 Best Local Similarity 17.2%; Pred. No. 0.11; Mismatches 159; Conservative 120; Indels 319; Gaps 39; Matches 159;

QY 48 KVAKPKTNKTMQISAEEGISAEGIQIVVKITDQGYVTSHGHDHYFYNGK--VPMDA 100  
 QY 101 I-----ISEELIMTDPN---YHFQSDVINEILGYVIK--- 132  
 Db 487 KQKADANNKV-QAFSQVGIVSGRSTLVNLNDDKQWDPNSIYFGFRGGRLLNGNSLTDFH 544  
 QY 545 IRNIDDGARVNHNMNTSNTITGESLITNPNTITSYNEAQD----DDHPLRIRSI 598

---

QY 133 -----NGNYVVLKPGSKRKNI-----RTKQQIAEQVAKGTKEAK 167  
 Db 599 PYROLYFNQDNRSYVTKKGASTRSEL,PONGESENWLYMGRRTSDAAKRVMNHINNER 658  
 QY 168 EKGLAQVAHLSEEVAVNEAK-----RQGRYTTDDGYIFSPPTDIIDDL---GDA 214  
 Db 659 MNGFN-GYFGEETKATONGKLNVTNGKSDQNRLFLTGG---TNLNGDLNVEKGTL 711  
 QY 215 YL---VPHGNHYHYI--PKKD--LSPSELAAAQAYWSOKQGARGPSDYRPTPAPGRRK 266  
 Db 712 FLSGRPTPHARDIAGISSTKKDPHFTENNEVVEDDWINR-----NEK 754  
 QY 267 APIPDVTNPQGQHQPQDNGGYHPAPPNDASQNKHORDEFKGKTFKELDQLHRLDLKY 326  
 Db 787 VHT---GYKTGDTIVCSRSDYTGVTCHNSNLSEKALNSFNPTN----LRGNVNLTE 836  
 QY 387 GSDHSKPSDKEVTHFLGHRRIKAYGKGLDGKPYDTSDAYFSKESIHSVDKSGVTAHKGD 446  
 Db 837 AS-----FTLGKANLFG--TIQSIGHTSQVNLKENS 864  
 QY 447 HFHYIGFGELEQYELDEVANWVKAKGQADELVAALDQEKGKEPLFDTRKVSRKVTKDGK 506  
 Db 865 HWHLTGNSNNVNLNLNTNGHHLNAQNDANKVTT-----YNTLTVN----- 904  
 QY 507 VGYIMPDKGKDYFARYQOLDLQIAFAEQUELMKDKHHYRYDIVDTGIEPRLAVIDVSSL 566  
 Db 905 ----SLSGNGSFY--YWDFT-----NNKSN-----KVVNKSA-- 932  
 QY 567 MHAGNATYDTGSSFVIPHIDHIIHWVPPSWLTRLRQIATI-----KYYMQHFEVRP 615  
 Db 933 --TGNFTLQVADKTGEPNHNELTLEFDASNATRNLEVTLANGSVDRGAWKYKLNRNGRY 990  
 QY 616 DVWSKPGHEEGSVIPN--VTPLDKRAKGMWNQWIHSAAEVOKALAEGRFAAPDGYIFD 672  
 Db 991 DLYN-PEVEKRNOTVDTTNITPPNDIOADAPSAQ--SNNEELARVETPVPPPAP----A 1042  
 QY 673 PRDVLAKEFFVWKDGFSFSPRAD---GSSLRTINKSDL---SQAEWQOQELLA 720  
 Db 1043 TESAIASEQPETRPAETAQPAMEETNTANSTETAPKSDTATQTENPNSESVPSETTEKVA 1102  
 QY 721 K-----KNAGDATD-----TDKP-----EEOQOAQDSNENQQPSEAS 752  
 Db 1103 ENPQOENETWAKNEQEATEPTPONGEVAKEDQPTVEANTQTNEATQSEGKTEETOTAK 1162  
 QY 753 KEEKESSDDFTDSLDPYGLDRATLEDHINQLAOKANID-----PKYLIFQP 797  
 Db 1163 SEPTESVTVSENOPEKTVSOSTEDKVVVEKEEKAVETEETQAKPQVTSKEPPKQAEPA 1222  
 QY 798 EGVOFYNKNGELVTYDIKTLQQINP 822  
 Db 1223 EFVP-TDTNAE---EAQALQOTP 1242

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/10661A  
 FILING DATE: 16-AUG-1995  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/296,791  
 FILING DATE: 25-AUG-1994  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Trecartin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: FP-59941/RFT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1848 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 PCT-US95-10661A-6

Query Match  
 Best Local Similarity 3.0%; Score 130.5; DB 5; Length 1848;  
 Matches 159; Conservative 17.2%; Pred. No. 0.11; Mismatches 327; Indels 319; Gaps 39;

Qy 48 KVAKAPKTKNTMDQIQAEEGISAEGISAEQIVVKITDQGYVTSQHGDHYHYNGK---VPYDA 100  
 Db 487 KOKADANNKV--QAFSQVGIVSGRSTLVNDDQKVDPNSIVFGFRGRDLINGNSLTFDH 544  
 Qy 101 I-----I-----ISELLMTDPN---YHFQSDVINEILDGYVIKV-- 132  
 Db 545 IRNIDDGARVWNHNMNTSNTITGESLITNPNTITSYNEAQD----DDPLRIRSI 598  
 Qy 133 -----NGNYVVYLKPGSKRKNI-----RTKQQIAEQVAKGTKEAK 167  
 Db 599 PYRQLYFNQDNRSYTLKKGASTRSELQPONGESNESNEWLYMGRRTSDAAKRNMVNHHINNER 658

Qy 168 EKGLAQVAHLSKEEVAVNEAK-----RQGRYTDDGYIFFSPTTDIDL---GDA 214

Db 659 MNGFN--GYFGEETEKTATQNGKLNVTFNGKSDQNRFLLTGG---TNLNGDLNVEKGTL 711  
 Qy 215 YL---VPHGNHYHI--PKKQ--LSPSELAAAQAYWSQOKQGRGARPSDYRPTPAPGRRK 266  
 Db 712 FLSGRPTPHARDIAGISSTKKDPHFTENNEVVEDDWINR-----NFK 754  
 Qy 267 APIPDVTTPNPGQGHQPDNGGYHAPPAPRNDAQNKHORDEFKGKTFKELLDQHLRLDKY 326  
 Db 755 ATTMNVVTGNASL-----YSGRNVANITSNITASNNAQ 786

Qy 327 RHEEDGLIFEPTQVIKSNAFGYVPHGDHYHIIPRSQLSPELEMALADRYLAGQTDNDS 386  
 Db 787 VHI--GYKTGDTVCVRSDYTGVTCHNSNLSEKALNSFNPTN-----LRGNVNLTE 836  
 Qy 387 GSDHSKPSDKEVTHFLGHRIKAYGKGLDGKPYDTSDAYVESKESTHSVDKSGVTAKHD 446  
 Db 837 AS-----AS-----FTLGKANLFG--TIQSIGTSSQVLKENS 864  
 Qy 447 HFHYTGEGELEQYELDEVANWVKAKGOADELVAALDQEQQGKEKPLFDTKKVSRVTKDGK 506  
 Db 865 HWHLTGNSNVNQNLNLNGHTHLNAQNDANKVTT-----YNFLTVN----- 904

Qy 507 VGYIMPKDGKDIFYARYQOLDTQIAFAEQEOLMLDKKKHYRDIVDTGIEPRLAVDVSSL 566

Db 905 -----SLSGNGSFY--YWVDFT-----NNKSN-----KVVNKSA-- 932  
 Qy 567 MHAGNATYDTGSSFVIPHDHIVVVPYSWLTRNQIATI-----KVVMQHPEVRP 615

RESULT 13  
 US-08-663-112-2  
 Sequence 2, Application US/08663112  
 Patent No. 5849503  
 GENERAL INFORMATION:  
 APPLICANT: WAGATSUMA, Masako  
 TITLE OF INVENTION: MUTANT PROTEINS OF HUMAN DNA  
 TITLE OF INVENTION: TOPOISOMERASE I  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/663,112  
 FILING DATE: 26-NOV-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Einaudi, Carolyn P.  
 REGISTRATION NUMBER: 32,220  
 REFERENCE/DOCKET NUMBER: 06609.1488-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 765 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-663-112-2

Query Match  
 Best Local Similarity 3.0%; Score 130; DB 2; Length 765;  
 Matches 155; Conservative 19.2%; Pred. No. 0.03; Mismatches 264; Indels 280; Gaps 40;  
 Qy 86 GDHVHFYNGKVPYDAIISELLMTDPNYH-FKOSDVINEILDGYVIVKVNQHPEVRP 144

Db 3 GDHLH-----NDSOIEADFRLNDSHKKDKHKDRREHRKE-----HKKEKORE 45  
 Qy 145 KRKNIRTKQQIAEQVAKGTFKEAKEKGGLAQVAHLSK-----EEVAVNEAKRQR 193  
 Db 46 KSKHNSNEHKDSEKKHEKEKTKHDKDKDRKEKKEEVRAASGDAKI-K 103  
 Qy 194 YTTDDGYIFSPTDIIDD-LGDAYLVPHGNHYHYPKKDLSPSELAAQAYWSQOKGRAR 252  
 Db 104 KEKENGF-SSPPOIKDEPEDGYFVP-----PKEDIP-----LKRPRDED 143  
 Qy 253 PSDYRP-----TPAPGRRKAPIPDVTNPNGQHQPDNGGGYHAPPNPDASQNKHQD 305  
 Db 144 DVDPKPKKIKTEBTKKEKKRKL-----EEEDGKLKPKPNKDKDKKVPEPDNKPKKKE 199  
 Qy 306 EFKGKTFKELLDOLHRLDKYRVEEDGLIFEPT-----QVIK-----343  
 Db 200 EOKWKKWEE---ERYPEGIKWKFLEHKGPFAPPYPLPENVKFYDGKVMKLPKAEV 256  
 Qy 344 SNAFGYVVPH-----GDHYHIIIPRSQLSPLLEMELADRYLAGQTD 382  
 Db 257 ATFFAKMLDHEYTITKELEFRKNFFKDWRKEMTNEERNNTI-TNLSCDFTQMSQYFAQTE 314  
 Qy 383 DNDSGSDHSKPSDKEVHTHFLGHRKAYGKGLDGKPYDTSAYVFEST-HSVDKSGV 440  
 Db 315 ARKOMSKEEKLKIKEENEKLL---KEYG-----FC1MDNH--KERIANFKTEPPGL 360  
 Qy 441 TAKHGDDHFHYIGFGELEQYELDEVANWVAKGQADELV-AALDQEKGKEKPLFDTKKV- 497  
 Db 361 FRGRGNH-----PKMGLKRRIMPEDITINCSKDAVKVSPPPGHKWKEVR 405  
 Qy 498 -SRKV-----KDGKVGYIM-----PKDGKDYFYARYQOLDLTQIAFAEQELML 539  
 Db 406 HDNKVUTWLVSWTENIQLGSQKIVMLNPNSSRIKGEKDWWQYETAR-----RLKKCVD 455  
 Qy 540 KDKKHYRDIVDTGIEPR---LAVDVSSLPMHAGN-----ATYDTGS-SFVIPHID- 586  
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 Qy 587 -----HIHWVPSWLRNQIATIKYVMQHPEVRPDWNSKPGHEESGSVTPNTPLDKRA 641  
 Db 516 PELDGQEYVVEFDFFLGKD--SIRY-----NKVPUVEKRV- 547  
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 Qy 700 RTINKSDLSQAQOELLAKKNAGDATTDKPEEK-----QQ 738  
 Db 590 RTENASTILQ--QQLKELTA-----PDENIPAKILSYNRANRAVAILCNHQR 634  
 Qy 739 A-----DKSNENOOQSEASKEEKESD 759  
 Db 635 APPKTFEEKSMMLQTKIDAKKEQOLAD 660  
 RESULT 14  
 US-08-488-940-2  
 Sequence 2, Application US/08488940  
 Patent No. 5854049  
 GENERAL INFORMATION:  
 APPLICANT: Reed, Guy L.  
 TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,940  
 FILING DATE: 09-JUN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER: 05433/009001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1181 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ; US-08-488-940-2  
 Query Match 3.0%; Score 129; DB 2; Length 1181;  
 Best Local Similarity 18.8%; Pred. No. 0.071;  
 Matches 180; Conservative 131; Mismatches 325; Indels 322; Gaps 49;  
 Matches 180; Conservative 131; Mismatches 325; Indels 322; Gaps 49;  
 Qy 29 HMGLATKDQIAVDDSKG-----VAKPNTNKTMQDQISAEGTSAEQIWKITDQGYVTS 84  
 Db 204 HMN-ADTDYSIAAFNKGEMATMINGPWAWSNIDTSKVNVGVT---VLPTFKGQPSK 257  
 Qy 85 HGDHYHYNGKVPYDALISEELIMTPNHYFQSDVINEILDGYVIVKNGNNYVYLKPGS 144  
 Db 258 -----PVGVVLASGINAASP-----KELAKEFLENYLTDG----LEAVN 295  
 Db 296 KDKPLGAVALKSYYEELAKDPRIAATMENAOKGEIMPNIPQMSAFWYAVRTAVINA-S 353  
 Qy 145 KRKNIR-TKQQIAEQVAK-----GTKEAKEKG--LAQWAHLS---KEEVAVNEAKRQ 191  
 Db 354 GRQTVDEA-----LKDQTNSSSSVPGRS 377  
 Qy 252 RPSDYRPTPAFGRKAPI-----DVTNPNGQGHOPDNGGYHPA 290  
 Db 378 -----IEGRNNSQLVNSVAGTVEGTNQDISLKFETDLTSRPAHGGKTEQGLSPKS 428  
 Qy 291 PPRPNDAQNKHORDEFKGKTFKELLDQL---HRLD-----LKYRH 328  
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 Qy 387 GSDHSKPSDKE-----VTHTFLGHRKAYGKGLDGKPYDTSAYFSKESIHSVDS 438  
 Db 542 ---FRPLKDTKLKTLAIGDTITSQELLAQAOQASILKNH--PGY---TIYERDSS 589  
 Qy 439 GVTAKHGDHFHYIGFGELEQYELDEVANW VKAKGOADELVALIDQEQGKEKPLFDTKKV 497  
 Db 590 IVT-HDNDIFRTI-----LPMDQEFTYRKNRQA---YRINKKGLNEEINNTDLI 637  
 Qy 498 SRKVTKDGKVGYIMPKDGKD-----FYARY-QLDLTQIAFAEQEQLMLDKKHYR 546  
 Db 638 SEKY-----YVLLKGKEPKYDPFDRSHLKLFTIKVYDVTNLKSEQLLTASERNLDF 690  
 Qy 547 YDIVDTGIEPLRAVDVSSLPMHAGNATYDTGSSFVIPHIDHIVVVPWSLT----- 597  
 Db 691 RDLYD-----PRDKAKLILY-----NLDARGIMDYT-LTGKVEDNHD 727  
 Qy 598 RNQIATIKYVMQHPE-----VRPDVWSKPGHE-----ESGSVTPNTPLDKRA 642

us-09-645-835a-6.raii

Mon Dec 3 07:54:20 2001

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Db 783 -NSOLVVSV---AGTVEGTNQDISLKFEE-IDLTSRPAHGGKTEOGLSPKSKPFATDSG 836
QY 697 SSLRTINKSDLSQAEMQAOELLAKKN-----AGDATTDKPEEKQADKSNE 745
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QY 746 QOPSEASKE-----EK-----ESDDFTIDSPLPDYGLDR 772
Db 894 TLPTQPVQFELLSGHVRVRYKEPKIQNQAKSVDVEYTQVFTPLNPDDDFRPGLKDTKL-- 951
QY 773 ATLEDHINQLAQKANIDPKYLIFQPE-----GVQFYNKNGELVTDIKTLQQINP 822
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RESULT 15
5231168-2
;Patent No. 5231168
; APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;
; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.
; TITLE OF INVENTION: MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409, 658
; FILING DATE: 18-SEP-1989
; SEQ ID NO:2:
; LENGTH: 783
; 5231168-2

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Best Local Similarity 18.3%; Pred. No. 0.049; Mismatches 294; Indels 281; Gaps 42;
Matches 159; Conservative 137; Mismatches 294; Indels 281; Gaps 42;

QY 41 YIDDSKGKVAKPTNKTMQDQISAEEG-----ISABQIVVKITDQGYVTSHGDH 88
Db 2 FVESEKSEHEAEN---EESSLEEGHHEEVPEONNEESEGESKLVDNDDEGGFEEAHHEN 57
QY 89 Y---HFYNGKVPYDAIISEELLMDPNYHFKQSDVINEILDGYVIKVNNGYYVYLPGSKR 146
Db 58 FSSEVSNSELNEFVESDKSVTEPAEH---EEVSE-----ESNPEAENEESSTI 105
QY 147 KNIRTQOQIAEQAQKGTKEAKEKGLAQVAHLSKEEVAAVNEAKROGRYTTDDGYIFSPTD 206
Db 106 EEAHQEEIVPEQ---NDEESGESGLVD-----NE---EGDFEEPNHEEFPDQ 147
QY 207 TIDDLGDAYLWPH-----GNHYHYIPKKDLS-PSE-----LAAQAYWSQKOG 248
Db 148 NDSELSENLVESEKSVSEPAEHVEI VSEKSVSEPAEHVEI VSEVSEQ 207
QY 249 RGARPSDYRPTAPGRRKAPIPDVTNNPG---QGHQPDNGGYHAPPNDAS----- 298
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QY 299 ---ONKHQDEFGKTFKELLQDLHRLLDKYRHEEDGLIFEPTQVIKNSAFGYVVPHG 354
Db 268 VPSEENKHASVDPEVKE-KENVSEV-----VEEKONSQESVEETPVNE----- 309
QY 355 DHYHITPRSQLSPLLEMELADRYLAGQTDDNSGSDHSKPS--DKEVTHFLGHRKAYC 411
Db 310 DEFEDVHTEQLD-----LDHTKTVDPPEIVEETPSELHENEVAH----- 348
QY 412 KGLDGKPYDTSAYVFSK-----ESIHSDVKSGVTAKHGDHFHYIGFGELEQYELDEV 464
Db 349 -----PEIVEIEEVFPERNQNNEFQEINEDDKSA-----HI-----QHETVEV 386
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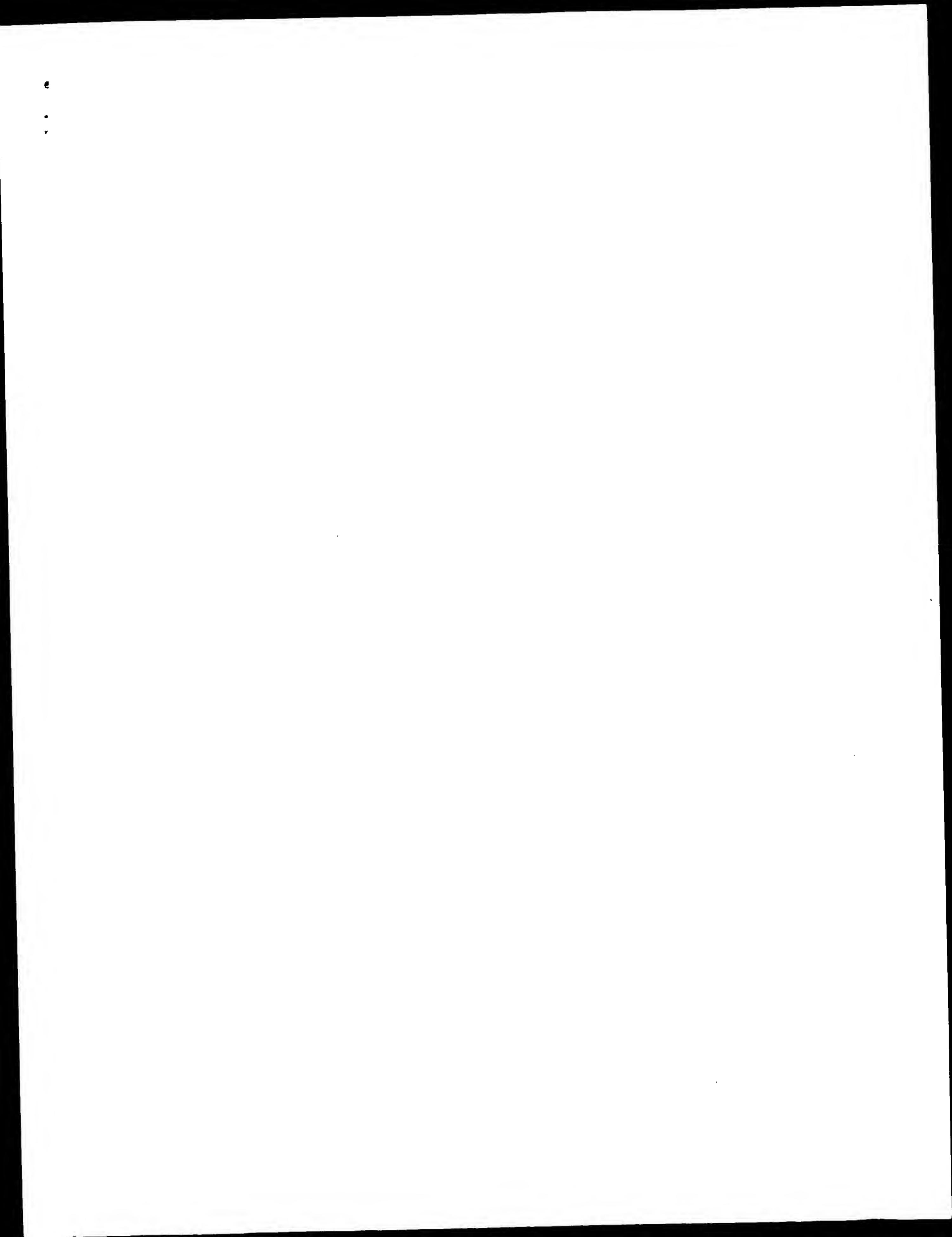
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QY 583 PHIDHIVWVFSWLTRNOIATIKY-VMQHPEVRPDVWSKGHEESGSVIPNVTPLDKRAG 641
Db 462 VEVEEI-----LPEDKNEKEVEHEIVEEELPEDKNEKGQH-EVEI-EELPEDK-- 510
QY 642 MPNWQIITHSAEEVQKALAEGRFAAPDGYIFDPRDVLAKEFVWKDGFSIPRA---- 696
Db 511 --NEKVOHETVEEELPEDKNEKGQH-EVEI-EELPEDKNEKGQH-EVEI-EELPEDK-- 567
QY 697 -----SSLRTINKSDLSQAEMQAOELL-----AKKNAGDATTDKPE 734
Db 568 KNEKVOHETVEEELPEDKNEKGQH-EVEI-EELPEDKNEKGQH-EVEI-EELPEDK-- 627
QY 735 EKQOADSNSNQQPSEASKEEKSDDFIDSPLPDYGLDRATEHDHINQLAQKANIDPKYLI 794
Db 628 ERK-----NEFSVEEK-----A1P0-----EPVPTLNENENVTPK-- 658
QY 795 FPPEGVQFYNKNGELVTD---IKTLQQINP 822
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Search completed: December 3, 2001, 07:16:20  
 Job time: 149 sec

Mon Dec 3 07:54:20 2001

us-09-645-835a-6.rai



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 3, 2001, 07:22:27 ; Search time 370.05 Seconds  
(without alignments)  
616.766 Million cell updates/sec

Title: US-09-645-835a-6

Perfect score: 4363

Sequence: 1 VKKTYGYIGSVAAILLATHI..... YNKNGELVTYDIKTLOQINP 822

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main :\*

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2: /cgn2\_6/ptodata/2/paa/US06\_COMBO.pep:\*

3: /cgn2\_6/ptodata/2/paa/US07\_COMBO.pep:\*

4: /cgn2\_6/ptodata/2/paa/US080\_COMBO.pep:\*

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24: /cgn2\_6/ptodata/2/paa/US60\_COMBO.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4363	100.0	822	1 PCT-US00-23417-6	Sequence 6, Appli
2	4363	100.0	822	20 US-09-645-835-6	Sequence 6, Appli
3	4363	100.0	822	20 US-09-645-835a-6	Sequence 6, Appli
4	4312.5	98.8	824	18 US-09-471-255-83	Sequence 83, Appli
5	4308	98.7	823	18 US-09-471-255-81	Sequence 81, Appli
6	4283.5	98.2	825	1 PCT-US00-23417-2	Sequence 2, Appli
7	4283.5	98.2	825	20 US-09-645-835-2	Sequence 2, Appli
8	4283.5	98.2	825	20 US-09-645-835a-2	Sequence 2, Appli
9	4157	95.3	793	16 US-09-252-088B-15	Sequence 15, Appli

## ALIGNMENTS

RESULT 1  
PCT-US00-23417-6  
; Sequence 6, Application PC/TUS0023417  
; GENERAL INFORMATION:  
; APPLICANT: Heinrichs, Jon  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Koenig, Scott  
; APPLICANT: Adamou, John E.  
; TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
; TITLE OF INVENTION: Vaccines  
; FILE REFERENCE: 469201-402  
; CURRENT APPLICATION NUMBER: PCT/US00/23417  
; CURRENT FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: U.S. 60/150,750  
; PRIORITY FILING DATE: 1999-08-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 822  
; TYPE: PRT  
; ORGANISM: Streptococcus agalactiae  
; PCT-US00-23417-6

Query Match 100.0%; Score 4363; DB 1; Length 822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDNOQIAVYIDDSSKGKVAKPTNKTMDQ 60

Qy 61 ISAEEGISAEOIVVKITDQGYVTSHGDHYHFYNGKVPYDAITISEELLMTDPNYHFKOSDV 120  
 ; ORGANISM: Streptococcus agalactiae  
 ; US-09-645-835-6

Db 61 ISAEEGISAEOIVVKITDQGYVTSHGDHYHFYNGKVPYDAITISEELLMTDPNYHFKOSDV 120

Qy 121 INEILDGYVIKVNGNYVYLKPGSKRKNIRTQQIAEQVAKGTKEAKEKGGLAQAHLIKE 180  
 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 INEILDGYVIKVNGNYVYLKPGSKRKNIRTQQIAEQVAKGTKEAKEKGGLAQAHLIKE 180

Qy 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPNGHNYHIPKKDLSPSELAAQ 240  
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 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPNGHNYHIPKKDLSPSELAAQ 240

Qy 241 AYWSQOKGRGARPSDYRPTPAPGRRKAPIPDVTNPNGHQPQDNGGYHPAPPNPDASQN 300  
 ; Query Match 100.0%; Score 4363; DB 20; Length 822;  
 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 AYWSQOKGRGARPSDYRPTPAPGRRKAPIPDVTNPNGHQPQDNGGYHPAPPNPDASQN 300

Qy 301 KHQREDFGKTFKELLDQLHRLDKYRHEEDGLIFEPTQVIKNSAFGYVPHGDHYHII 360  
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 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 PRSQLSPLMELADRYLAGOTDDNSGSDHSKPSDEKVTHTFLGHRKAYGKGLDGKPYD 420

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 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 481 LDQEQQEKPLFDTKVSRSKVTKGKVGYIMPQDGKDIFYARYQOLDTQIAFAEQLMLK 540

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 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 541 DKKHYRYDIVDTGIEPRLAVIDVSSLPMHAGNATYDTGSSFVIPHIDIHVWPYSWLTRNQ 600

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 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 601 IATIKYVMQHPEVRPVDSKPGHEESGSVIPNVTPLDKRAGMPNWQOIHSAEEVQKALAE 660

Qy 661 GRFAAAPDGYIFDPRDVLSKPGHEESGSVIPNVTPLDKRAGMPNWQOIHSAEEVQKALAE 720  
 ; Query Match 100.0%; Score 4363; DB 20; Length 822;  
 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 661 GRFAAAPDGYIFDPRDVLSKPGHEESGSVIPNVTPLDKRAGMPNWQOIHSAEEVQKALAE 720

Qy 721 KKNAGDATTDKPEEKQODKSNSENOQSEASKEEKEESDDFFIDSLSLPDGYGLDRATEDHIN 780  
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 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 721 KKNAGDATTDKPEEKQODKSNSENOQSEASKEEKEESDDFFIDSLSLPDGYGLDRATEDHIN 780

Qy 781 QLAQKANIDPKYLIFQPEGVQFYNKNGELVTDIKTLQQINP 822  
 ; Query Match 100.0%; Score 4363; DB 20; Length 822;  
 ; Best Local Similarity 100.0%; Pred. No. 0; Length 822;  
 ; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 781 QLAQKANIDPKYLIFQPEGVQFYNKNGELVTDIKTLQQINP 822

RESULT 2  
 US-09-645-835-6  
 Sequence 6, Application US/09645835  
 GENERAL INFORMATION:  
 APPLICANT: Heinrichs, Jon  
 APPLICANT: Johnson, Leslie S.  
 APPLICANT: Koenig, Scott  
 APPLICANT: Adamou, John E.  
 TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
 TITLE OF INVENTION: Vaccines  
 FILE REFERENCE: 469201-402  
 CURRENT APPLICATION NUMBER: US/09/645,835

CURRENT FILING DATE: 2000-08-25  
 PRIOR APPLICATION NUMBER: U.S. 60/150,750  
 PRIOR FILING DATE: 1999-08-25  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 6  
 LENGTH: 822  
 TYPE: PRT

RESULT 3  
 US-09-645-835A-6  
 Sequence 6, Application US/09645835A  
 GENERAL INFORMATION:  
 APPLICANT: Heinrichs, Jon  
 APPLICANT: Koenig, Scott  
 APPLICANT: Adamou, John E.

TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
 TITLE OF INVENTION: Vaccines  
 FILE REFERENCE: 469201-493  
 CURRENT APPLICATION NUMBER: US/09/645,835A  
 CURRENT FILING DATE: 2000-08-25  
 PRIOR APPLICATION NUMBER: U.S. 60/150,750  
 NUMBER OF SEQ ID NOS: 7  
 SEQ ID NO 6  
 SOFTWARE: PatentIn Ver. 2.1  
 LENGTH: 822  
 TYPE: PRT  
 ORGANISM: *Streptococcus agalactiae*  
 S-09-645-835A-6

Query	Match	Score	DB	Length
Y	1 VKKTYGYIGSVAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKVAPTKNTMDQ	100.0%	20;	822;
Y	1 VKKTYGYIGSVAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKVAPTKNTMDQ	100.0%	20;	822;
Y	61 ISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELMTDPNYHKQSDV	100.0%	20;	822;
Y	61 ISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELMTDPNYHKQSDV	100.0%	20;	822;
Y	121 INEILDGYVIKVNNGNYYVLKPGSKRKNIRTQOIAEQVAKGTKEAKEKGLAOVAHLSKE	100.0%	20;	822;
Y	121 INEILDGYVIKVNNGNYYVLKPGSKRKNIRTQOIAEQVAKGTKEAKEKGLAOVAHLSKE	100.0%	20;	822;
Y	181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHIPKKDLSPSELAAQ	98.9%	20;	822;
Y	181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHIPKKDLSPSELAAQ	98.9%	20;	822;
Y	241 AYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPQGHOPDNGGYHPAPPRPNDASQ	98.9%	20;	822;
Y	241 AYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPQGHOPDNGGYHPAPPRPNDASQ	98.9%	20;	822;
Y	301 KHQREDFKGKTFKELLDQHLRDLKRYRVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHI	98.9%	20;	822;
Y	301 KHQREDFKGKTFKELLDQHLRDLKRYRVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHI	98.9%	20;	822;
Y	361 PRSQLSPLEMELADRYLAGOTDDNSGSDHSKPSDKEVTHFLGRIKAYGKGLDGPYD	98.9%	20;	822;
Y	361 PRSQLSPLEMELADRYLAGOTDDNSGSDHSKPSDKEVTHFLGRIKAYGKGLDGPYD	98.9%	20;	822;
Y	421 TSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELVA	98.9%	20;	822;
Y	421 TSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELVA	98.9%	20;	822;
Y	481 LDQEOKGKEKPLFDTKVKSRKVTKDGKVGYIMPMDGKDYFYARYQDLTQIAFAEQELMLK	98.9%	20;	822;
Y	481 LDQEOKGKEKPLFDTKVKSRKVTKDGKVGYIMPMDGKDYFYARYQDLTQIAFAEQELMLK	98.9%	20;	822;
Y	541 DKKHYRYDIVDTGIEPRALDVSSSLPMHAGNATDTGSSFVIPHIDHIIHVWPYSWLTRNO	98.9%	20;	822;
Y	541 DKKHYRYDIVDTGIEPRALDVSSSLPMHAGNATDTGSSFVIPHIDHIIHVWPYSWLTRNO	98.9%	20;	822;
Y	601 IATIKYVMOHPEVRPDVWPKPGHEESGSVIPNVTPLDKRAGMPNWQIITHSAEEVQKALAE	98.9%	20;	822;
Y	601 IATIKYVMOHPEVRPDVWPKPGHEESGSVIPNVTPLDKRAGMPNWQIITHSAEEVQKALAE	98.9%	20;	822;
Y	661 GRFAAPDGYIEDPRDVLAKETFWKDGFSFIPRADGSSLRTINKSDLQSOAEWQQAELLA	98.9%	20;	822;
Y	661 GRFAAPDGYIEDPRDVLAKETFWKDGFSFIPRADGSSLRTINKSDLQSOAEWQQAELLA	98.9%	20;	822;
Y	721 KKNAGDATTDKPEEKQOADSNEQQPSEASKEEKESDDFIDSLLPDPYGLDRATELEDHIN	98.9%	20;	822;
Y	721 KKNAGDATTDKPEEKQOADSNEQQPSEASKEEKESDDFIDSLLPDPYGLDRATELEDHIN	98.9%	20;	822;
Y	781 QLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP	98.9%	20;	822;

RESULT 4  
 US-09-471-255-83  
 ; Sequence 83, Application US/09471255  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BIOCHEM PHARMA INC.  
 ; APPLICANT: HAMEL, Jos,e  
 ; APPLICANT: BRODEUR, Bernard R.  
 ; APPLICANT: PINEAU, Isabelle  
 ; APPLICANT: MARTIN, Denis  
 ; APPLICANT: RIOUX, Cl'ment  
 ; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
 ; FILE REFERENCE: 12806-11PCT  
 ; CURRENT APPLICATION NUMBER: US/09/471, 255  
 ; CURRENT FILING DATE: 1998-12-23  
 ; NUMBER OF SEQ ID NOS: 102  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; LENGTH: 824  
 ; TYPE: PRT  
 ; ORGANISM: S. pneumoniae  
 ; US-09-471-255-83

Query Match Score DB Length  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Score DB Length  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 814; Conservative 98.9%; Mismatches 3; Indels 1; Gaps 1;

Qy 1 VKKTYGYIGSVAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKVAPTKNTMDQ

Db 1 VKKTYGYIGSVAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKVAPTKNTMDQ

Qy 61 ISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELMTDPNYHKQSDV

Db 61 ISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELMTDPNYHKQSDV

Qy 121 INEILDGYVIKVNNGNYYVLKPGSKRKNIRTQOIAEQVAKGTKEAKEKGLAOVAHLSKE

Db 121 INEILDGYVIKVNNGNYYVLKPGSKRKNIRTQOIAEQVAKGTKEAKEKGLAOVAHLSKE

Qy 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHIPKKDLSPSELAAQ

Db 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHIPKKDLSPSELAAQ

Qy 241 AYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPQGHOPDNGGYHPAPPRPNDASQ

Db 241 AYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPQGHOPDNGGYHPAPPRPNDASQ

Qy 301 KHQREDFKGKTFKELLDQHLRDLKRYRVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHI

Db 301 KHQREDFKGKTFKELLDQHLRDLKRYRVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHI

Qy 361 PRSQLSPLEMELADRYLAGOTDDNSGSDHSKPSDKEVTHFLGRIKAYGKGLDGPYD

Db 361 PRSQLSPLEMELADRYLAGOTDDNSGSDHSKPSDKEVTHFLGRIKAYGKGLDGPYD

Qy 421 TSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELVA

Db 421 TSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELVA

Qy 481 LDQEOKGKEKPLFDTKVKSRKVTKDGKVGYIMPMDGKDYFYARYQDLTQIAFAEQELMLK

Db 481 LDQEOKGKEKPLFDTKVKSRKVTKDGKVGYIMPMDGKDYFYARYQDLTQIAFAEQELMLK

Qy 541 DKKHYRYDIVDTGIEPRALDVSSSLPMHAGNATDTGSSFVIPHIDHIIHVWPYSWLTRNO

Db 541 DKKHYRYDIVDTGIEPRALDVSSSLPMHAGNATDTGSSFVIPHIDHIIHVWPYSWLTRNO

Qy 601 IATIKYVMOHPEVRPDVWPKPGHEESGSVIPNVTPLDKRAGMPNWQIITHSAEEVQKALAE

Db 601 IATIKYVMOHPEVRPDVWPKPGHEESGSVIPNVTPLDKRAGMPNWQIITHSAEEVQKALAE

Qy 661 GRFAAPDGYIEDPRDVLAKETFWKDGFSFIPRADGSSLRTINKSDLQSOAEWQQAELLA

Db 661 GRFAAPDGYIEDPRDVLAKETFWKDGFSFIPRADGSSLRTINKSDLQSOAEWQQAELLA

Qy 721 KKNAGDATTDKPEEKQOADSNEQQPSEASKEEKESDDFIDSLLPDPYGLDRATELEDHIN

Db 721 KKNAGDATTDKPEEKQOADSNEQQPSEASKEEKESDDFIDSLLPDPYGLDRATELEDHIN

Qy 781 QLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP

Db 781 QLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP

QY 601 IATIKYVMQHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQIITHSAEEVKALAE 660  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 601 IATIKYVMQHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQIITHSAEEVKALAE 660  
QY 661 GRFAAPDGYIFDPDRDVLAKETFWKDGFSFSIPRADGSSLRTINKSDLSQAEWQQAQELLA 720  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 661 GRFATPDGYIFDPDRDVLAKETFWKDGFSFSIPRADGSSLRTINKSDLSQAEWQQAQELLA 720  
QY 721 KKNAGDATDDKPEEKQADKSNEQQPSEASK-EKESEDFFIDSLSLPDYGLDRATEDHN 779  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 721 KKNAGDATDDKPEEKQADKSNEQQPSEASKEEKESESDDFFIDSLSLPDYGLDRATEDHN 780  
QY 780 NOLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP 822  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 781 NOLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP 823

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RESULT 5  
;US-09-471-255-81  
; Sequence 81, Application US/09471255  
; GENERAL INFORMATION:  
; APPLICANT: BIOCHEM PHARMA INC.  
; APPLICANT: HAMEL, JOS, e  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: PINEAU, Isabelle  
; APPLICANT: MARTIN, Denis  
; APPLICANT: RIOUX, Clment  
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
; FILE REFERENCE: 12806-11PCT  
; CURRENT APPLICATION NUMBER: US/09/471, 255  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/113, 800  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 81  
; LENGTH: 823  
; TYPE: PRT  
; ORGANISM: S. pneumoniae  
; US-09-471-255-81

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Query Match 98.7%; Score 4308; DB 18; Length 823;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 810; Conservative 6; Mismatches 0; Gaps 0;

QY 1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDQNQIAVYIDDSDKGVVKAPTKNTMDQ 60  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDQNQIAVYIDDSDKGVVKAPTKNTMDQ 60  
QY 61 ISAAEGISAEQIVVKITDOGYVTSHGHDHYHYFNGKVPYDAIISEELLMTDPNYHKQSDV 120  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 61 ISAAEGISAEQIVVKITDOGYVTSHGHDHYHYFNGKVPYDAIISEELLMTDPNYRFKQSDV 120

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Query Match 98.2%; Score 4283.5; DB 1; Length 825;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 810; Conservative 6; Mismatches 6; Indels 3; Gaps 2;

QY 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLPHGNHYHYIPKKDLSPSELAAQ 240  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLPHGNHYHYIPKKDLSPSELAAQ 240  
QY 241 AYWSOKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPGQGHQPDNGGYHPAPPNNDASQN 300  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 241 AYWSOKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPGQGHQPDNGGYHPAPPNNDASQN 300  
QY 301 KHQRDEFKGKTFKELLDQLHLRDLKRYRWEEDGLIFEPTQVIKSNAGFGYVPHGDHYHI 360  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 301 KHQRDEFKGKTFKELLDQLHLRDLKRYRWEEDGLIFEPTQVIKSNAGFGYVPHGDHYHI 360

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QY 361 PRSQLSPLEMLADRYLAGQTDNDSGSDHSKPSDKEVTHFLGRRIKAYGKGLDGKPYD 420  
;|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I  
;Db 361 PRSQLSPLEMLADRYLAGQTDNDSGSEHSKPSDKEVTHFLGRRIKAYGKGLDGKPYD 420

QY 241 AYWSQOKQGRGARPSDYRPT--PAPGRRKAPIPDVTNPQGHOPDNGGYHPAPPNPDAS 298  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 241 AYWSQOKQGRGARPSDYRPTPAPGRRKAPIPDVTNPQGHOPDNGGYHPAPPNPDAS 300  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 299 QNKHQREDFKGKTFKELLDQLHLRDLKYRHEEDGLIFEPTQVIKSNAFGYVPHGDHYH 358  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 301 QNKHQREDFKGKTFKELLDQLHLRDLKYRHEEDGLIFEPTQVIKSNAFGYVPHGDHYH 360  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 359 IIPRSQSLPLEMELADRYLAGTDDNDGSDSHKPSDKEVTHFLGHRIKAYGKGLDGKP 418  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 361 IIPRSQSLPLEMELADRYLAGTDDNDGSDSHKPSDKEVTHFLGHRIKAYGKGLDGKP 420  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 419 YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADEVLY 478  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 421 YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELA 480  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 479 AALDQEQQKEKPLFDTKVSRKVTKGKVGYMPKDKDGFYARQOLDTOTFAEQELM 538  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 481 AALDQEQQKEKPLFDTKVSRKVTKGKVGYMPKDKDGFYARQOLDTOTFAEQELM 540  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 539 LKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGNATYTGSSFVIPHIDHTHWVPSWLTR 598  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 541 LKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGNATYTGSSFVIPHIDHTHWVPSWLTR 600  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 599 NQIATIKYVMOHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQIHSAAEVOKAL 658  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 601 DQIATIKYVMOHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQIHSAAEVOKAL 660  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 659 AEGRFAAPDGYIFDPRDVLAKETFWKDGFSIIPRADGSSLRTINKSDLSQAEWQQAEL 718  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 661 AEGRFAAPDGYIFDPRDVLAKETFWKDGFSIIPRADGSSLRTINKSDLSQAEWQQAEL 720  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 719 LAKKNAGDATTDKPEEKQOADSNSENQOPSEASK-EEKESDDFIDSLSLPDYGLDRATED 777  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 721 LAKKNAGDATTDKPEEKQOADSNSENQOPSEASKEEKEESDDFIDSLSLPDYGLDRATED 780  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 778 HINOLAQKANIDPKYLIFOPEGVQFYNKNGELVTDIKTLQOINP 822  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 781 HINOLAQKANIDPKYLIFOPEGVQFYNKNGELVTDIKTLQOINP 825  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 RESULT 7  
 US-09-645-835-2  
 ; Sequence 2, Application US/09645835  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heinrichs, Jon  
 ; APPLICANT: Johnson, Leslie S.  
 ; APPLICANT: Koenig, Scott  
 ; APPLICANT: Adamou, John E.  
 ; TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
 ; FILE REFERENCE: 469201-402  
 ; CURRENT APPLICATION NUMBER: US/09/645, 835  
 ; CURRENT FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: U.S. 60/150, 750  
 ; PRIORITY FILING DATE: 1999-08-25  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 825  
 ; TYPE: PRT  
 ; ORGANISM: Streptococcus pyogenes  
 ; US-09-645-835-2  
 Query Match 98.2%; Score 4283.5; DB 20; Length 825;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 810; Conservative 6; Mismatches 6; Indels 3; Gaps 2;  
 QY 1 VKKTYGYIGSVAILLATHIGSYOLGKHHMLATKDNQIAYIDDSKGKVAKPTNKTMDO 60  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 1 VKKTYGYIGSVAILLATHIGSYOLGKHHMGSATKDNOIAYIDDSKGKAKPTNKTMDO 60  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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QY 61 ISAAEGISAEQIVWKITDQGYVTSHGDHYHFYNGKVPYDAISEELIMTDPNYHFKQSDV 120  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 61 ISAAEGISAEQIVWKITDQGYVTSHGDHYHFYNGKVPYDAISEELIMTDPNYHFKQSDV 120  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 121 INEILDGYVIKVNGNYVVLPGSKRNIRTQKQIAEQVAKGTKEAKEKGKLAQVAHLSKE 180  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 121 INEILDGYVIKVNGNYVVLPGSKRNIRTQKQIAEQVAKGTKEAKEKGKLAQVAHLSKE 180  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 181 EVAAVNEAKRQGRYTTDDGYIFSPTDTIIDLGLDAYLVPNGHNYHIPPKKDLSPSELAAQ 240  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 181 EVAAVNEAKRQGRYTTDDGYIFSPTDTIIDLGLDAYLVPNGHNYHIPPKKDLSPSELAAQ 240  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 241 AYWSQOKQGRGARPSDYRPT--PAPGRRKAPIPDVTNPQGQHOPDNGGYHPAPPNPDAS 298  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 241 AYWSQOKQGRGARPSDYRPTPAPGRRKAPIPDVTNPQGQHOPDNGGYHPAPPNPDAS 300  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 299 QNKHQREDFKGKTFKELLDQLHLRDLKYRHEEDGLIFEPTQVIKSNAFGYVPHGDHYH 358  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 301 QNKHQREDFKGKTFKELLDQLHLRDLKYRHEEDGLIFEPTQVIKSNAFGYVPHGDHYH 360  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 359 IIPRSQSLPLEMELADRYLAGTDDNDGSDSHKPSDKEVTHFLGHRIKAYGKGLDGKP 418  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 361 IIPRSQSLPLEMELADRYLAGTDDNDGSDSHKPSDKEVTHFLGHRIKAYGKGLDGKP 420  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 419 YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADEVLY 478  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 421 YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELA 480  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 479 AALDQEQQKEKPLFDTKVSRKVTKGKVGYMPKDKDGFYARQOLDTOTFAEQELM 538  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 481 AALDQEQQKEKPLFDTKVSRKVTKGKVGYMPKDKDGFYARQOLDTOTFAEQELM 540  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 539 LKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGNATYTGSSFVIPHIDHTHWVPSWLTR 598  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 541 LKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGNATYTGSSFVIPHIDHTHWVPSWLTR 600  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 599 NQIATIKYVMOHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQIHSAAEVOKAL 658  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 601 DQIATIKYVMOHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQIHSAAEVOKAL 660  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 659 AEGRFAAPDGYIFDPRDVLAKETFWKDGFSIIPRADGSSLRTINKSDLSQAEWQQAEL 718  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 661 AEGRFAAPDGYIFDPRDVLAKETFWKDGFSIIPRADGSSLRTINKSDLSQAEWQQAEL 720  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 719 LAKKNAGDATTDKPEEKQOADSNSENQOPSEASK-EEKESDDFIDSLSLPDYGLDRATED 777  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 721 LAKKNAGDATTDKPEEKQOADSNSENQOPSEASKEEKEESDDFIDSLSLPDYGLDRATED 780  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 778 HINOLAQKANIDPKYLIFOPEGVQFYNKNGELVTDIKTLQOINP 822  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 781 HINOLAQKANIDPKYLIFOPEGVQFYNKNGELVTDIKTLQOINP 825  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 RESULT 8  
 US-09-645-835A-2  
 ; Sequence 2, Application US/09645835A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heinrichs, Jon  
 ; APPLICANT: Johnson, Leslie S.  
 ; APPLICANT: Koenig, Scott  
 ; APPLICANT: Adamou, John E.  
 ; TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for  
 ; FILE REFERENCE: 469201-493  
 ; CURRENT APPLICATION NUMBER: US/09/645, 835A  
 ; CURRENT FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: U.S. 60/150, 750  
 ; PRIORITY FILING DATE: 1999-08-25  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 825

TYPE: PRT  
 ORGANISM: *streptococcus pyogenes*  
 US-09-645-835a-2

APPLICANT: CHARLEBOIS, Isabelle  
 APPLICANT: HAMEL, Jose  
 APPLICANT: MARTIN, Denis  
 TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS

.

CURRENT APPLICATION NUMBER: US/09/252,088  
 CURRENT FILING DATE: 1999-02-18  
 EARLIER APPLICATION NUMBER: US/60/075,425  
 FILE REFERENCE: 8331-9002  
 NUMBER OF SEQ ID NOS: 44  
 SEQ ID NO 15  
 LENGTH: 793  
 SOFTWARE: Patentin Ver. 2.0

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TYPE: PRT  
 ORGANISM: group B streptococcus

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Query Match 98.2%; Score 4283.5; DB 20; Length 825;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 810; Conservative 6; Mismatches 6; Indels 3; Gaps 2;  
 QY 1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDQNQIAYIDDSDKGVVKAPTKNTMDQ 60  
 Db 1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGSATKDQNQIAYIDDSDKGVVKAPTKNTMDQ 60  
 QY 61 ISAEEGISAEQIVWVKTIDQGYVTSHGDHYHFYNGKPYDAIISEELLMTDPNYHEKOSDV 120  
 Db 61 ISAEEGISAEQIVWVKTIDQGYVTSHGDHYHFYNGKPYDAIISEELLMTDPNYHEKOSDV 120  
 QY 121 INEILDGYVIKVNGNYYVYLPGSKRKNIRTQOIAEQVAKGTKEAKEKGGLAQVHLSKE 180  
 Db 121 INEILDGYVIKVNGNYYVYLPGSKRKNIRTQOIAEQVAKGTKEAKEKGGLAQVHLSKE 180  
 QY 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIDDLGDAYLVPNGHNYHYPKKDLSPSELAAQ 240  
 Db 181 EVAAVNEAKRQGRYTTDDGYIFSPTDIDDLGDAYLVPNGHNYHYPKKDLSPSELAAQ 240  
 QY 241 AYWSQKQGRGARPSDYRPT-PAPGRRKAPIPDVTNPQGQHQPDNGGYHAPPORNDA 298  
 Db 241 AYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTNPQGQHQPDNGGYHAPPORNDA 300  
 QY 299 QNKHQREDFGKTFKELLDQLHLRDLKYRVEEDGLIFEPTQVIKSNAGFYVVPNGDHYH 358  
 Db 301 QNKHQREDFGKTFKELLDQLHLRDLKYRVEEDGLIFEPTQVIKSNAGFYVVPNGDHYH 360  
 QY 359 IIPRSQSLPLEMELADRYLAGQTDDNDSSDHSKPSDKEVTHFLGHRRIKAYGKGLDGK 418  
 Db 361 IIPRSQSLPLEMELADRYLAGQTDDNDSSDHSKPSDKEVTHFLGHRRIKAYGKGLDGK 420  
 QY 419 YDTSDAYVFSEKSIHSVDSKGVTAKHGDHFHYIGFGELEQYELDEVANWVAKGQADELV 478  
 Db 421 YDTSDAYVFSEKSIHSVDSKGVTAKHGDHFHYIGFGELEQYELDEVANWVAKGQADELV 480  
 QY 479 AALDQEKGKEPLFDTKVKSRKVTKDGKVGYIMPKDGKDIFYARYQOLDLTQIAFAEOLM 538  
 Db 481 AALDQEKGKEPLFDTKVKSRKVTKDGKVGYIMPKDGKDIFYARDQDLTQIAFAEOLM 540  
 QY 539 LDKKKHYRDIVDTGIEPRLAVIDVSSLPMHAGNATYDTGSSFVIPHIDHTHVVPSWLTR 598  
 Db 541 LDKKKHYRDIVDTGIEPRLAVIDVSSLPMHAGNATYDTGSSFVIPHIDHTHVVPSWLTR 598  
 QY 599 NQIATIKYVMQHPEVRPDVWWSKGHEESGSVIPNVTPLDKRAGMPNQIILHSAEEVOKAL 600  
 Db 601 DOIATIKYVMQHPEVRPDVWWSKGHEESGSVIPNVTPLDKRAGMPNQIILHSAEEVOKAL 600  
 QY 659 AEGRAAEPGYIFPDRVLAKETFWWDGSFSIPRADGSSLRTINKSDLQAEOQAEL 718  
 Db 661 AEGRAAEPGYIFPDRVLAKETFWWDGSFSIPRADGSSLRTINKSDLQAEOQAEL 720  
 QY 719 LAKKNAGDATDTKPEEKQADKSNEQOPSEASK-EEKESDDFDISLPLDYGLDRATED 777  
 Db 721 LAKKNAGDATDTKPEEKQADKSNEQOPSEASKEEESDDFDISLPLDYGLDRATED 780  
 QY 778 HINOLAOKANIDPKYLIFQPEGVQFYNGELVTDIKTLQOINP 822  
 Db 781 HINOLAOKANIDPKYLIFQPEGVQFYNGELVTDIKTLQOINP 825

Query Match 95.3%; Score 4157; DB 16; Length 793;  
 Best Local Similarity 95.3%; Pred. No. 0;  
 Matches 781; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 30 MGLATKDQNQIAYIDDSDKGVVKAPTKNTMDQIISAEEGISAEQIVWVKTIDQGYVTSHGDHY 60  
 Db 1 MGLATKDQNQIAYIDDSDKGVVKAPTKNTMDQIISAEEGISAEQIVWVKTIDQGYVTSHGDHY 60  
 QY 90 HFYNGKVPYDAIISEELLMTDPNYHFQOSDWINEILDGYVIKVNGNYYVYLPGSKRNI 149  
 Db 61 HFYNGKVPYDAIISEELLMTDPNYRFQOSDWINEILDGYVIKVNGNYYVYLPGSKRNI 120  
 QY 150 RTKQOIAEQVAKGTKEAKEKGGLAQVHLSKE 180  
 Db 121 RTKQOIAEQVAKGTKEAKEKGGLAQVHLSKE 180  
 QY 210 DLGDAYLVPNGHNYHYPKKDLSPSELAAQAWSQKQGRGARPSDYRPTPAPGRRKAPI 269  
 Db 181 DLGDAYLVPNGHNYHYPKKDLSPSELAAQAWSQKQGRGARPSDYRPTPAPGRRKAPI 240  
 QY 270 PDVTPNPGQGQHQPDNGGYHAPPORNDAQNKHQRDEFGKTFKELLDQLHLRDLKYRH 329  
 Db 241 PDVTPNPGQGQHQPDNGGYHAPPORNDAQNKHQRDEFGKTFKELLDQLHLRDLKYRH 300  
 QY 330 EEDGLIFEPTQVIKSNAGFYVVPNGDHYHITPRSQLPLEMELADRYLAGQTDDNDSSD 389  
 Db 301 EEDGLIFEPTQVIKSNAGFYVVPNGDHYHITPRSQLPLEMELADRYLAGQTDDNDSSD 360  
 QY 390 HSKPSDKEVTHFLGHRRIKAYGKGLDGKPYTSDAYVFSEKSIHSVDSKGVTAKHGDHFH 449  
 Db 361 HSKPSDKEVTHFLGHRRIKAYGKGLDGKPYTSDAYVFSEKSIHSVDSKGVTAKHGDHFH 420  
 QY 450 YIGFGELEQYELDEVANWVAKGQADELVALDQEKGKEPLFDTKVKSRKVTKDGKVGY 509  
 Db 421 YIGFGELEQYELDEVANWVAKGQADELVALDQEKGKEPLFDTKVKSRKVTKDGKVGY 480  
 QY 510 IMPKDGKDIFYARYQOLDLTQIAFAEOLMLKDKKKHYRDIVDTGIEPRLAVIDVSSLPMH 569  
 Db 481 IMPKDGKDIFYARYQOLDLTQIAFAEOLMLKDKKKHYRDIVDTGIEPRLAVIDVSSLPMH 540  
 QY 570 GNATYDTGSSFVIPHIDHTHVVPSWLTRNQIATIKYVMQHPEVRPDVWWSKGHEESGSV 629  
 Db 541 GNATYDTGSSFVIPHIDHTHVVPSWLTRNQIATIKYVMQHPEVRPDVWWSKGHEESGSV 600  
 QY 630 IPNVTPLDKRAGMPNQIILHSAEEVOKALAEGRFAAEPGYIFPDRVLAKETFWWDGSF 689  
 Db 661 SIPRADGSSLRTINKSDLQAEOQAEL 660  
 QY 750 EASKEEESDDFDISLPLDYGLDRATEDHINOLAOKANIDPKYLIFQPEGVQFYNGEL 809  
 Db 721 EASKEEESDDFDISLPLDYGLDRATEDHINOLAOKANIDPKYLIFQPEGVQFYNGEL 780

RESULT 9

US-09-252-088-15

; Sequence 15, Application US/0925088

; GENERAL INFORMATION:

; APPLECTANT: BRODEUR, Bernard R.

; APPLECTANT: RIOUX, Clement

; APPLECTANT: BOYER, Martine

QY 810 VTYDIKTLQQINP 822  
Db 781 VTYDIKTLQQINP 793

RESULT 10  
US-09-252-088B-15  
; Sequence 15, Application US/09252088B  
; GENERAL INFORMATION:  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: BOYER, Martine  
; APPLICANT: CHARLEBOIS, Isabelle  
; APPLICANT: HAMEL, Josee  
APPLICANT: MARTIN, Denis  
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 8331-9002  
CURRENT APPLICATION NUMBER: US/09/252, 088B  
CURRENT FILING DATE: 1999-02-18  
PRIORITY NUMBER: US/60/075, 425  
PRIORITY FILING DATE: 1998-02-20  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 793  
TYPE: PRT  
ORGANISM: group B streptococcus  
US-09-252-088B-15

Query Match 95.3%; Score 4157; DB 16; Length 793;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 781; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 30 MGLATKDQNQIAYIDDSKGKVAKPTNKTMQDQISAEEGISAETVWKTMDGYVITSHGDHY 89  
Db 1 MGLATKDQNQIAYIDDSKGKVAKPTNKTMQDQISAEEGISAETVWKTMDGYVITSHGDHY 60

QY 90 HFYNGKVPYDAITSEELLMTDPNYHFKQSDVINEILDGYVIVKVNNGNYYVYLPGSKRKNI 149  
Db 61 HFYNGKVPYDAIISSEELLMTDPNYRFQSDVINEILDGYVIVKVNNGNYYVYLPGSKRKNI 120

QY 150 RTKQQIAEQVAKGKTEAKEKGKLAQVHLSKEEVAAVNEAKRQGRYTDDGYIFSPPTDID 209  
Db 121 RTKQQIAEQVAKGKTEAKEKGKLAQVHLSKEEVAAVNEAKRQGRYTDDGYIFSPPTDID 180

QY 210 DLGDAYLVPNGHNYHVKKKDLSPSELAAQAYWSQKQGRGARPSDYRPTPAPGRRKAPI 269  
Db 181 DLGDAYLVPNGHNYHVKKKDLSPSELAAQAYWSQKQGRGARPSDYRPTPAPGRRKAPI 240

QY 270 PDVTNPNGHQPDNGGYHAPPRNDASQNKHORDEFKGKTFKELLDQLHLRDLKYRH 329  
Db 241 PDVTNPNGHQPDNGGYHAPPRNDASQNKHORDEFKGKTFKELLDQLHLRDLKYRH 300

QY 330 EEDGLIFEPTQVIKSNAFGYVPHGDHYHIPSQSLSPLEMELADRYLAGQTDDNDGSD 389  
Db 301 EEDGLIFEPTQVIKSNAFGYVPHGDHYHIPSQSLSPLEMELADRYLAGQTDDNDGSD 360

QY 390 HSKPSDKEVHTFLGHRIKAYKGKLDGKPYDTS DAYFSKESIH SVDKSGVTAKHGDHFH 449  
Db 361 HSKPSDKEVHTFLGHRIKAYKGKLDGKPYDTS DAYFSKESIH SVDKSGVTAKHGDHFH 420

QY 450 YIGFGELEQYELDEVANWVKAKGQADELVAALDQEQQKEKPLFDTKVSRKVTKDGKVGY 509  
Db 421 YIGFGELEQYELDEVANWVKAKGQADELVAALDQEQQKEKPLFDTKVSRKVTKDGKVGY 480

QY 510 IMPKGDKDYFYARYQQLDTQIAFAOEMLKDKHHYRDIVTGIPEPLAVDVSSLPMHA 569  
Db 481 MMPKGDKDYFYARDQQLDTQIAFAOEMLKDKHHYRDIVTGIPEPLAVDVSSLPMHA 540

QY 570 GNATYDTGSSFVIPHIDHIIHVVPYSWLTRNOIATIKYVMQHPEVRPDVWSKPGHEESGSV 629  
Db 781 VTYDIKTLQQINP 793

RESULT 11  
US-09-252-088-16  
; Sequence 16, Application US/09252088  
; GENERAL INFORMATION:  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: RIoux, Clement  
; APPLICANT: BOYER, Martine  
; APPLICANT: CHARLEBOIS, Isabelle  
; APPLICANT: HAMEL, Jose  
APPLICANT: MARTIN, Denis  
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 8331-9002  
CURRENT APPLICATION NUMBER: US/09/252, 088B  
CURRENT FILING DATE: 1999-02-18  
EARLIER APPLICATION NUMBER: US/60/075, 425  
EARLIER FILING DATE: 1998-02-20  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 715  
TYPE: PRT  
ORGANISM: group B streptococcus  
US-09-252-088-16

Query Match 86.1%; Score 3758; DB 16; Length 715;  
Best Local Similarity 98.5%; Pred. No. 2.9e-299;  
Matches 704; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 108 MTDPNYHFKQSDVINEILDGYVIVKVNNGNYYVYLPGSKRKNI RTKQQIAEQVAKGKTEAK 167  
Db 1 MTDPNYRFQSDVINEILDGYVIVKVNNGNYYVYLPGSKRKNI RTKQQIAEQVAKGKTEAK 60

QY 168 EKGLAQVHLSKEEVAAVNEAKRQGRYTDDGYIFSPPTDIDDLGDAYLVPNGHNYHYP 227  
Db 61 EKGLAQVHLSKEEVAAVNEAKRQGRYTDDGYIFSPPTDIDDLGDAYLVPNGHNYHYP 120

QY 228 KKDLSPELAAQAYWSQKQGRGARPSDYRPTPAPGRRKAPI PDVTNPNGHQPDNGGY 287  
Db 121 KKDLSPELAAQAYWSQKQGRGARPSDYRPTPAPGRRKAPI PDVTNPNGHQPDNGGY 180

QY 288 HPAPPRNDASQNKHORDEFKGKTFKELLDQLHLRDLKYRHVEEDGLIFEPTQVIKSNAF 347  
Db 181 HPAPPRNDASQNKHORDEFKGKTFKELLDQLHLRDLKYRHVEEDGLIFEPTQVIKSNAF 240

QY 348 GYWVPHGDHYHIPSQSLSPLEMELADRYLAGQTDDNDGSDHSKPSDKEYTHFLGHRI 407  
Db 241 GYWVPHGDHYHIPSQSLSPLEMELADRYLAGQTDDNDGSEHHSKPDSKEVHTFLGHRI 300

QY 408 KAYKGKLDGKPYDTS DAYFSKESIH SVDKSGVTAKHGDHFHYIGFGELEQYELDEVANW 467  
Db 301 KAYKGKLDGKPYDTS DAYFSKESIH SVDKSGVTAKHGDHFHYIGFGELEQYELDEVANW 360

QY 468 VKAKGQADELVAALDQEQQKEKPLFDTKVSRKVTKDGKVGY IMPKGDKDYFYARYQQLD 527

RESULT 12  
US-09-252-088B-16  
; Sequence 16, Application US/09252088B  
; GENERAL INFORMATION:  
; APPLICANT: BRODEUR, Bernard R.  
; APPLICANT: RIOUX, Clement  
; APPLICANT: BOYER, Martine  
; APPLICANT: CHARLEBOIS, Isabelle  
; APPLICANT: HAMEL, Josee  
; APPLICANT: MARTIN, Denis  
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS  
FILE REFERENCE: 8331-9002  
CURRENT APPLICATION NUMBER: US/09/252, 088B  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US/60/075, 425  
PRIORITY FILING DATE: 1998-02-20  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 715  
TYPE: PRT  
ORGANISM: group B streptococcus  
US-09-252-088B-16

Query Match 86.1%; Score 3758; DB 16; Length 715;  
Best Local Similarity 98.5%; Pred. No. 2.9e-299; Mismatches 704; Conservative 6; Indels 0; Gaps 0;

QY 108 MTDPNYHFKOSDVINEILDGYVIKVNGNYYVYLPGSKRKKNIRTQQIAEQVAKGTEAK 167  
Db 1 MTDPNYRFQKOSDVINEILDGYVIKVNGNYYVYLPGSKRKKNIRTQQIAEQVAKGTEAK 60

QY 168 EKGLAQVHLSEKEVAEVNEAKRQGRYTTDDGYIFSPPTDITDDLGDAYLVPFGHNYHYIP 227  
Db 61 EKGLAQVHLSEKEVAEVNEAKRQGRYTTDDGYIFSPTDIIDDLDAYLVPFGHNYHYIP 120

QY 228 KKLSPSELAAQWYSQKQGRGARPSDYRPTAPGRRKAPIPDVTNPQGHOPDNGY 287  
Db 121 KKLSPSELAAQWYSQKQGRGARPSDYRPTAPGRRKAPIPDVTNPQGHOPDNGY 180

QY 288 HPAPPRNDASONKHQRDEFKGKTFKELLDOLHRLDKYRVEDGLIFEPTQVKSNAF 347  
Db 181 HPAPPRNDASONKHQRDEFKGKTFKELLDOLHRLDKYRVEDGLIFEPTQVKSNAF 240

QY 348 GYWVPHGDHYHILPRSQLSPLLEMELADRYLAGTDDNSGSDHSKPSDKEVTHFLGRI 407  
Db 241 GYVVPHGDHYHILPRSQLSPLLEMELADRYLAGTDDNSGSEHSKPSDKEVTHFLGRI 300

QY 408 KAYKGKLDGKPYDTSDAYVFSKEIHSVDKSGVTAKHGDHFHYIGFGELEQEYELDEVANW 467  
Db 301 KAYGKGLDGKPYDTS DAYVFSKEIHSVDKSGVTAKHGDHFHYIGFGELEQEYELDEVANW 360

QY 468 VKAKGQADELVAALDQEQQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDVFYARYQOLDL 527  
Db 361 VKAKGQADELAAALDQEQQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDVFYARYQOLDL 420

QY 588 IHVVPYSWLTRNQIATIKYVMQHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQI 647  
Db 481 IHVVPYSWLTRDQIATVKYVMQHPEVRPDVWSKGHEESGSVIPNVTPLDKRAGMPNWQI 540

QY 648 IHSAAEVQKALAEGRAAPDGYIFDPRDVLAKEFVWKDGFSIPRADGSSLRTINKSDL 707  
Db 541 IHSAAEVQKALAEGRAAPDGYIFDPRDVLAKEFVWKDGFSIPRADGSSLRTINKSDL 600

QY 708 SQAEMQQAQELLAKKNAGDATDTKPEEKQADKSNEQQPSEASKEESESDDFIDS LPD 767  
Db 601 SQAEMQQAQELLAKKNAGDATDTKPEEKQADKSNEQQPSEASKEESESDDFIDS LPD 660

QY 768 YGLDRATEDHINQLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP 822  
Db 661 YGLDRATEDHINQLAQKANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLOQINP 715

RESULT 13  
US-09-468-656-10  
; Sequence 10, Application US/09468656  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Koenig, Scott  
; APPLICANT: Adamou, John E.  
TITLE OF INVENTION: Streptococcus Pneumoniae and Immunogenic Fragments for Vaccines  
FILE REFERENCE: 469201-444  
CURRENT APPLICATION NUMBER: US/09/468, 656  
CURRENT FILING DATE: 1999-12-21  
EARLIER APPLICATION NUMBER: 60/113, 048  
EARLIER FILING DATE: 1998-12-21  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 819  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-468-656-10

Query Match 24.2%; Score 1054; DB 18; Length 819;  
Best Local Similarity 33.6%; Pred. No. 7.9e-77; Mismatches 295; Conservative 103; Mismatches 235; Indels 246; Gaps 34;

QY 1 VKKTYGYIGSVAILLATHIGSYQLGKHHMLATKD-NQIAYIDDSSKGKVAKPTNKTM 59  
Db 3 INKKY-LAGSVA-VLALSVCSELGRYQAGQDKKESNRRAVIDGDQAGQKA-ENLTPD 57

QY 60 QISAEGGISEAQIVVKITDQGYVTSHGHDHYHYNGKVPYDAIISEELLMIDPNVHFQSD 119  
Db 58 EVSKREGINAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDAIISEELLMKDPNQQLKDS 117

QY 120 VINEILDGYVIKVNGNYYVYLPGSKRKKNIRTQQIAEQVAKGTEAKEKGLAQVHL SK 179  
Db 118 IVNEIKGGYVIKVNGNYYVYLKGDAHADNIRKKEIKRQ---KQERSH----HNSR 167

QY 180 EVAEVNEAKRQGRYTTDDGYIFSPPTDITDDLGDAYLVPFGHNYHYIPKKDLSP SELAA 239  
Db 168 AD-NAVAARAQGRYTTDDGYIFNASDIEDTGDAYIVPHGDHYHYIPKNELSAELAA 226

QY 240 QAYWSQKQGRGARPSDYRPTAPGRRKAPIPDVTNPQGHOPDNGGYHPAPPRNDASQ 299

Db 227 EAYWNGKQ--GSRPSSSSSYNA-----NPAQPRLSENHNLTWT----- 263  
 Qy 300 NKHQRDEFKGKTFKELLDOLHRLDKYRVEEDGLIFEPTQVIKSNAGFYVVPHDHYHI 359  
 Db 264 TYHQN--QGENISSLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHF 320  
 Qy 360 IPRSQLSPELEMAD---RYLAG-----QTDDNDSGSDHSKPSDKEVTHTF 402  
 Db 321 IPYEQMSLELEKRIARIPLRYRSNHWFEDSRPEEPSQPTPEPSPSPOPAPSNP----- 374  
 Qy 403 LGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKGVTAKHGDHFHYIGFELEQYELD 462  
 Db 375 -----IDGK-----LVKEAVRKV-----GDGY-----VFEEN 396  
 Qy 463 EVANWVKAKGQADELVAALDQEOGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDYFYAR 522  
 Db 397 GVSRYIPAKDLDSAETAAGIDSKLAKQESL--SHKLGTKKTD-----LPSSDREFYNKA 447  
 Qy 523 YQLDLTQIAFAEQELMLDKKKHYRDIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVI 582  
 Db 448 YDL---LARIHQDLDNKGRQVDFEALDNLE-RLK-DVSS----- 483  
 Qy 583 PHTDHTHWVPYSWLTRNQIATIKYVMQHPEVRPDVWSKPGHEEHSVIPNVTPLDKRAMG 642  
 Db 484 ---DKVKLV-----EDILAFLAPIRHPE-----RLGK 507  
 Qy 643 PNWOIILHSAEEWQKALAEGRFAAPPDGYIFDPDVLAKEFVWKDGGSFSIPRADGSSLRTI 702  
 Db 508 PNAQITYTDDEIQVAKLAGKYTAEDGYIFDPDRDITSDE----GDAYVTPHMTHS--HWI 560  
 Qy 703 NKSDSLSQLAQELLAKKNAGDATDDKPEEKQQADKSNEENOQSEA--SKEEKESDD 760  
 Db 561 KKDSLSEAERAQAYAEEKGL-----TPPSTDHQDSGNTEAKGAEAIYNRVKAKKV 613  
 Qy 761 FIDSLP-----DYGLDRA---TLEDHINOLAQKA 786  
 Db 614 PLDRMPYLNQYTVEVKNGSLIIPHHDHYHNIKFEMFDEGLYEAPKGYTLLEDLLATV--- 669  
 Qy 787 NIDPKYLIFQP-----EGVQFYNKNGELVT 811  
 Db 670 ---KYYVEHPNERPHSDNGFGNASDHVQ-RNKNGQADT 703

RESULT 14  
 US-09-471-255-99  
 Sequence 99, Application US/09471255  
 GENERAL INFORMATION:  
 APPLICANT: BIOCHEM PHARMA INC.  
 APPLICANT: HAMEL, Jos,e  
 APPLICANT: BRODEUR, Bernard R.  
 APPLICANT: PINEAU, Isabelle  
 APPLICANT: MARTIN, Denis  
 APPLICANT: RIOUX, CL,ment  
 TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS  
 FILE REFERENCE: 12806-11PCT  
 CURRENT APPLICATION NUMBER: US/09/471,255  
 CURRENT FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: US 60/113,800  
 PRIOR FILING DATE: 1998-12-23  
 NUMBER OF SEQ ID NOS: 102  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 99  
 LENGTH: 811  
 TYPE: PRT  
 ORGANISM: S. pneumoniae

S-09-471-255-99

```

QY 22 SYQLGKHMLATKD-NQIAYIDDSKGKVAPKTNKTMDQISAEEGISAEOIVVKITDOG 80
Db 2 SVELGRHQAQVKRESNRVSYIDGDQAGOKA--ENLTPDEVSKEGINAEQIVIKITDQG 59
QY 81 YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFQSDVINEILDGYVIKVNGNYYVYL 140
Db 60 YVTSHGDHYHYNGKVPYDAIISEELLMKDPPNYQLKSDIVNEIKGGYVIKVDGKYYVYL 119
QY 141 KPGSKRKNTRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEEVAVNEAKROGRYTDDGY 200
Db 120 KDAAHADNIRTKEEIKRQ----KQERSHN----HNSRAD-NAVAARAQGRRYTDDGY 168
QY 201 IFSPPTIDDLGDAYLVPHGNHYHYPKKDLSPSELAAQAYWSOKQRGARPSDYRPTP 260
Db 169 IFNASDITEDTGDAYIVPHGDHYHYIPKSDLSASELAAQAYWNGKQ--GSRPSSSSHN 226
QY 261 APGRRKAPIPDVTNPQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLDQH 320
Db 227 A-----NPAQPRLSENHNLTVT-----TYHON---QGENTISSLLRELY 262
QY 321 RLDLKYRHVEEDGLIFEPTQVIKSNAFGYVWPQGDHYHITPRSQLSPELEMAD---RY 376
Db 263 AKPLSERHWESDGЛИFDPAQITSRTANGVAVPHGDHYHFIPYSQSLPLEEKЛАRIIPLRY 322
QY 377 LAG-----QTDDNDSGSDHSKPSDKEVTHTFLGHRRIKAYGKGLDGKPYDTS 423
Db 323 RSNHWVPDSRPEQSPSPQSTPEPPSPSPQAPNPQPA-----PSNPIDEK- 365
QY 424 AYVFSKESIHHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELVAALDQ 483
Db 366 ---LVKEAVRKV----GDGY-----VFEENGVPRYIPAKDLSAETAAGIDS 404
QY 484 EQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGYFYARYQOLDLTOIAFAEQELMLKDKK 543
Db 405 KLAQQESL-SHKLGAKKTD-----LPSSDREFYNKAYDL---LARIHQDLLDNKGR 451
QY 544 HYRYDIVDTGIEPRLAVDSSLPMHAGNATYDTGSSFVIPHDHIVVVPYSWLTRNQIAT 603
Db 452 QVDFEALDNLE-RLK-DVSS-----DKVKLV-----DDILA 481
QY 604 IKYVMQHPEVRPDVWSKPGHEEGSVIPNVTPLDKRAGMPNWQITHSAEEVQKALAEGRF 663
Db 482 FLAPIRHPE-----RLGKPNAQITYTDDETIQVAKLAGKY 515
QY 664 AAPDGYIFDPDRDVLAKETFVWKDGFSFSTPRADGSSLRTINKSDLSQAEWQQAQELLAKKN 723
Db 516 TTEDGYIFDPDRDITSDE----GDAYVTPHMTHS--HWIKKDSLSEAERAQQAYAKEKG 568
QY 724 AGDATDTDKPEEKQOADKSNNENQOPSEA 751
Db 569 L-----TPPSTDHQDSGNTEAKGAEA 589

RESULT 15
US-09-471-255-95
; Sequence 95, Application US/09471255
; GENERAL INFORMATION:
; APPLICANT: BIOCHEM PHARMA INC.
; APPLICANT: HAMEL, Jos, e
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: PINEAU, Isabelle
; APPLICANT: MARTIN, Denis
; APPLICANT: RIoux, Cl'ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471, 255
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113, 800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for windows Version 3.0
SEQ ID NO 95
LENGTH: 834

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TYPE: PRT  
ORGANISM: *S. pneumoniae*  
US-09-471-255-95

Search completed: December 3, 2001, 07:22:36  
Job time: 525 sec

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**OM protein - protein search, using sw model**

Run on: December 3, 2001, 07:16:20 ; Search time 39.47 Seconds  
(without alignments)  
465.231 Million cell updates/sec

Title: US-09-645-835A-7

Perfect score: 4265

Sequence: 1. MKINNKYLVGSAALILSVC.....KLLALLKGNSNPSSVSKEN 816

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cggn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cggn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

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4: /cggn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cggn2\_6/ptodata/2/iaa/pctus\_COMB.pep:\*

6: /cggn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match Length	DB	ID	Description
1	4163	97.6	796	4	US-08-961-083-56	Sequence 56, Appl
2	2661.5	62.4	763	4	US-08-961-083-56	Sequence 66, Appl
3	1186.5	27.8	447	4	US-08-961-083-56	Sequence 182, Appl
4	152	3.6	783	6	5231168	Patent No. 5231168
5	145.5	3.4	1073	4	US-09-541-782-6	Sequence 6, Appl
6	144	3.4	1040	4	US-08-961-083-118	Sequence 118, Appl
7	140	3.3	1503	4	US-08-976-255-14	Sequence 14, Appl
8	140	3.3	2431	1	US-07-920-281C-2	Sequence 2, Appl
9	140	3.3	2431	4	US-08-466-277-2	Sequence 2, Appl
10	135.5	3.2	740	1	US-08-257-073-5	Sequence 5, Appl
11	135.5	3.2	1183	2	US-08-447-031A-2	Sequence 2, Appl
12	135	3.2	2308	1	US-08-015-973-1	Sequence 1, Appl
13	135	3.2	2308	2	US-08-448-164-1	Sequence 1, Appl
14	135	3.2	2308	4	US-08-081-929-2	Sequence 2, Appl
15	133.5	3.1	1507	6	5268270-2	Patent No. 5268270
16	133.5	3.1	1664	2	US-08-642-846-2	Sequence 2, Appl
17	133	3.1	1093	5	PCT-US93-03077-1	Sequence 1, Appl
18	132	3.1	1338	1	US-08-471-033-50	Sequence 50, Appl
19	132	3.1	1338	2	US-08-471-044-50	Sequence 50, Appl
20	132	3.1	1338	2	US-08-463-483A-50	Sequence 50, Appl
21	132	3.1	1338	2	US-08-471-046A-50	Sequence 50, Appl
22	132	3.1	1338	2	US-08-470-566B-50	Sequence 50, Appl
23	132	3.1	1338	2	US-08-469-334-50	Sequence 50, Appl
24	132	3.1	1338	3	US-09-300-529-50	Sequence 50, Appl
25	130.5	3.1	1435	2	US-08-568-459A-4	Sequence 4, Appl
26	130.5	3.1	1435	2	US-08-487-826B-4	Sequence 4, Appl
27	130	3.0	2115	4	US-09-324-867-5	Sequence 5, Appl

**ALIGNMENTS**

RESULT	1
US-08-961-083-56	Sequence 56, Application US/08961083
	Patent No. 6159469
	GENERAL INFORMATION:
	APPLICANT: Choi et. al.
	TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
	NUMBER OF SEQUENCES: 452
	CORRESPONDENCE ADDRESS:
	ADDRESSEE: Human Genome Sciences, Inc.
	STREET: 9410 Key West Avenue
	CITY: Rockville
	STATE: Maryland
	COUNTRY: USA
	ZIP: 20850
	COMPUTER READABLE FORM:
	MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
	COMPUTER: HP Vectra 486/33
	OPERATING SYSTEM: MS DOS version 6.2
	SOFTWARE: ASCII Text
	CURRENT APPLICATION DATA:
	APPLICATION NUMBER: US/08/961,083
	FILING DATE:
	CLASSIFICATION: 435
	PRIOR APPLICATION DATA:
	APPLICATION NUMBER:
	FILING DATE:
	ATTORNEY/AGENT INFORMATION:
	NAME: Brookes, A. Anders
	REGISTRATION NUMBER: 36,373
	REFERENCE/DOCKET NUMBER: PB340P2
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: (301) 309-8504
	TELEFAX: (301) 309-8512
	INFORMATION FOR SEQ ID NO: 56:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 796 amino acids
	TYPE: amino acid
	STRANDEDNESS: single
	TOPOLOGY: linear
	MOLECULE TYPE: protein
	US-08-961-083-56

Query Match Similarity 97.6%; Score 4163; DB 4; Length 796;  
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Sequence 5, Appl

Qy 21 SYELGLYQARTVKENNRRVSYIDGKQATOKTENLTPDEVSKREGINAQIVIKLTDOGYVT 80

OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961, 083  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36, 373  
 REFERENCE/DOCKET NUMBER: PB340P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 66:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 763 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-961-083-66

Query Match 62.4%; Score 2661.5; DB 4; Length 763;  
 Best Local Similarity 66.8%; Pred. No. 1.4e-192; Indels 49; Gaps 8;  
 Matches 520; Conservative 78; Mismatches 131;

QY 20 CSYELGLYQARTV-KENNRVSYIDGKQATQKTTENLTPDEVSREGINAEOIVIKITDQY 78  
 Db 1 CSYELGRHQAGQVKKESENRSYIDGQAGQKAENLTDPDEVSREGINAEOQXVIKTDOY 60

QY 561 EGDAYVTPHMGSHWIGKDSLKEVAAQAYTEKEKGILPLSPADVKANPTGDSAAIY 620  
 Db 481 KEKLVDLLAFLAPITHPERLGKPNQSOIETYTEDEVRIAQALDKYTSDGYIFDEHDIIISD 540

QY 561 EGDAYVTPHMGSHWIGKDSLKEVAAQAYTEKEKGILPLSPADVKANPTGDSAAIY 620  
 Db 601 NRVKGEKRIPLVRLPYMVEHTVEKGNLIIIPHKDHYNIKFAWFDDHTYKAPNGYTL 660

QY 621 NRVKGEKRIPLVRLPYMVEHTVEKGNLIIIPHKDHYNIKFAWFDDHTYKAPNGYTL 680  
 Db 661 LFTAKYVTPHMGSHWIGKDSLSDKEVAAQAYTEKEKGILPLSPADVKANPTGDSAAIY 720

QY 681 LFTAKYVTPHMGSHWIGKDSLSDKEVAAQAYTEKEKGILPLSPADVKANPTGDSAAIY 740  
 Db 721 QVETEKVEAQLKEAVLAKVTDSLKANATELAGLRNNLTQIMDNNSIMAEEAKLLA 780

QY 801 LLKGSNPSSVSKEKIN 816  
 Db 781 LLKGSNPSSVSKEKIN 796

RESULT 2  
 US-08-961-083-66  
 Sequence 66, Application US/08961083  
 ; Patent No. 6159469  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Choi et. al.  
 ; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
 ; NUMBER OF SEQUENCES: 452  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 ; COMPUTER: HP Vectra 486/33

QY 675 GYTLEDLFATIKYVVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE----- 728  
Db 646 GYTLEDLLATVKYVVEHPNPERPHSDNGFGNASHVQRNKNGQADTNQTEKPSEEKPOTEK 705  
Qy 729 PVEET-----PAAPEPVPOVETEKVEAQLKEAEVLLAKVTD 763  
Db 706 PEETPREEKPOSEKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQD 763  
  
RESULT 3  
; Sequence 182, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 182:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 447 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-961-083-182  
  
Query Match 27.8%; Score 1186.5; DB 4; Length 447;  
Best Local Similarity 41.0%; Pred. No. 1.3e-81;  
Matches 263; Conservative 62; Mismatches 110; Indels 207; Gaps 11;  
QY 24 LGLYQARTVKENNRVSYIDGKQATQKTENLTPEVSKREGINAEQIVIKITDDGYVTSHG 83  
Db 1 LNOHQRSQENKDNNRVSYVDGSQSSQKSENLTQDQVSQEGIQAEQIVIKITDQGVTSHG 60  
QY 84 DHYHYNGKVPYDAITISEELLMDPNYKLKDEDIVNEVGKGGIVIKVDGKYYVYLKDAHA 143  
Db 61 DHYHYNGKVPYDALFSEELLMKDPNQYQLKDAH 120  
QY 144 DNVRTKEEINROKQEHQSQHREGGTPRNDGAVALARSGQRTDDGYIFNAASDIEDTGDA 203  
Db 121 DNVRTKEEINRQKQEHVKDNE---KVNSNAVARSQGRYTTNDGYVENPADIEDTGNA 176  
QY 204 YIVPHGDHYHYPKNELSASELAAEAFSLGRGNLSNSRTYRRQNSDNTSRINWVPSVN 263  
Db 177 YIVPHGGHYIPKSDLSASELAAKLAGKNMQPSQLSYSSTASDN----- 224  
  
QY 264 PGTTNTNTSNSNTNSQASQNSNDISLLKOLYKPLSQRHVESDGLVFDPAQITSRTARG 323  
Db 225 ---NTQSVAGKSTSCKPANKSENLOSLKELYDPSAQRYSESDGLVFDPAKIIISRTPNG 280  
QY 324 VAVPHGDHYHFLPYSMQSELEERIARIILPRYRSNHWPDSRPEOPSPQPTPEPPGPQP 383  
Db 281 VAIPHGDHYHFLPYSKLSALEEKIARMVP----- 309  
QY 384 APNLKIDSNSSLVSQLVRKVGEFYFEKGISRYFAKDLIPSETVKNLESKLSKQESVSH 443  
Db 310 ----ISGTGSTVSTNAK-----PNEVVSSLGSLSSNPSS--- 349  
QY 444 TLTAKKENVAPRDQEFYDKAYNLTEAHKALFENKGRNSDFQALDKLLERLNDESTNKEK 503  
Db 340 -LTTSKE-----LSSA-----SDGYIFNPKDIVEETAT 366  
QY 564 AVVTTPMHGHSHWIGKDSLSDKEVVAQAYTKEKGILPPSPDADVKAQ-----TGDSA 616  
Db 367 AYIVVRHGDHFHYI----PKSNOIGQOPTLPNNSLATPSPSLPI -NPGTSHEKHEEDY 418  
QY 617 AATYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYH 658  
Db 419 GF DANRIIAE-----DESGFVMSHGDHNH 442  
  
RESULT 4  
5231168-2  
; Patent No. 5231168  
; APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;  
; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.  
; TITLE OF INVENTION: MALARIA ANTIGEN  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/409, 658  
; FILING DATE: 18-SEP-1989  
; SEQ ID NO:2;  
; LENGTH: 783  
; SEQ ID NO:2;  
; LENGTH: 783  
; 5231168-2

Query Match 3.6%; Score 152; DB 6; Length 783;  
Best Local Similarity 20.3%; Pred. No. 0.0038;  
Matches 142; Conservative 106; Mismatches 277; Indels 174; Gaps 35;  
; Matches 263; Conservative 62; Mismatches 110; Indels 207; Gaps 11;  
QY 198 EDTGDAYIVPHGDHYHYPKNELSASELAAEAFSLGRGNLNSNSRTYRQ--NSDNTSRT 255  
Db 35 EESGESKLV-----DNEDEGFEAAHHENFSS---EVNSNELNEFVESDK--- 77  
QY 256 NWVPSVSNPGTTNTNTSNSNTNSQASQNSNDISLLKOLYKPLSQRHVES-DGLV--- 310  
Db 78 ---SVTEPAEEHVSEESNPEAENEESTEAEHOE-EIVPEONDEESEGESGLVDNE 131  
QY 311 -----FDPAQITS-----RTARGVAVPHGDHYHFLPYSMQSELEERIARIIL 351  
Db 132 EGDFEEPNEEEFPDQNDSELSENELVESEKSVEP-AEHVETVESEKSVEP-AEHV-EIV 189  
QY 352 PLRYRSNHWVPSRPEQSPQPTPERP--PGPQPAQNL---KIDSNSSLVSQLVRKV 404  
Db 190 SEKSTSE---PAEHVESVSEQSNNEPSEKKDGPVPSKPFEEIEKVDPQPKIVD-LQIIE 244  
QY 405 EGYF-----EERGISMVFAKDLPLSETVK-NLESKLKQESVSHTLAKK-----EN 451  
Db 245 PNFDSDQNPQEPVPSFKIEKVPSSEENKHASVDPVKEKENVSEVQNSQESVEE 304  
QY 452 VAPRDQEYDKAYNLITEAKA-----LFENKGRNSDFQALDKLLERLNDE 497  
Db 305 IPVNEDEFEDVHTEQLDLHDKTVDPEIVEVEEIPSELHNEVAHPEIVEEIPFPEPNQ 364

QY 498 STNKEKLVDDLLAFLA-PITHPERLGKPNQSOIETYDE-VRIAQOLADKYTTSDGYIFDEH 555  
Db 365 NEFOEINEDDKSAHQHEIVEELVEELLPEDDKNEKEVHEIVEELVEELPEKNEKG---OH 420  
Db 421 EIVEVE--EILPE-----DDKNEKEVHEIVEELP--EDKNEKKGHEIVE 463  
Db 464 VEELPEDKNEK-----VEHEIVEEVEELPNEKG----QHEIVE 463  
QY 556 DISDEGGDAYVTPHMGSHWIGKDSLSDKEVAAQAYTEKKGILPPSPDADVAKANTGDS 615  
Db 616 AAATYNRKGKRIPLVRLPYMVEH-TVEVKNGNLIPHKDHYHNKFAWFDDHTYKAPN 674  
Db 675 GYTLEDFATIKYYVEHPDE-RPHSNDGWNAS---EHVLGKKDHSE----- 717  
Db 504 EILPEDKNEKVQHEIVEVEELPEDKNEKEVQHEIVEELPEIVEELPEIVE 563  
QY 718 -DPNKNFKADEEPVEETPAEPEVPOVETEKVEAQLKEAVLLAKVTDSLKANATELAG 776  
Db 564 LPEDKNEKVQHEIVEVEELPEDKNEKEVQHEIVEELPEIVEELPEIVE 614  
QY 777 LRNNLTQIMDNNSIMAEAKLLALKGSNPSSVSKEKI 815  
Db 615 TNNNENIE-----TIKPEEK-----NEFSVEEKAI 640

RESULT 5  
US-09-541-782-6  
; Sequence 6, Application US/09541782  
; Patent No. 6284480  
; GENERAL INFORMATION:  
; APPLICANT: Nislow, Corey  
; APPLICANT: Sakowicz, Roman  
; APPLICANT: Beraud, Christophe  
; TITLE OF INVENTION: Antifungal Assay  
; FILE REFERENCE: 1015  
; CURRENT APPLICATION NUMBER: US/09/541,782  
; CURRENT FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1073  
; TYPE: PRT  
; ORGANISM: S.pombe  
; US-09-541-782-6

Query Match 3.4%; Score 145.5; DB 4; Length 1073;  
Best Local Similarity 18.6%; Pred. No. 0.019;  
Matches 182; Conservative 136; Mismatches 357; Indels 301; Gaps 41;

QY 43 GKOATQTKTENLTPDEVSKREGINAEE-----QIVIKI-TDOGYVTSHGDHYHYN 90  
Db 147 GOTGTGKTYTMSGD-LSDSDGILSEGAGLIPRALYQLFSSLNNSQEYAVK-CSYYELYN 204  
QY 91 GKVPYDAIISEELLMKDPMYKLKDED----TNEVKGGYVIKVDGKYYVYLKDAAHADN 145  
Db 205 EEI-RDLVSEEL--RKPARVFEDTSRRGNWVITGTEESY-IKNAGDGLRLREGSHRRQ 260  
QY 146 VRTKEEINRQKQEH-----OHREGGTPRNDGAVALRSQGRYTDGYIFNASDIEDT 200  
Db 261 VAATKCNDSLSSRSHSIFTLHRKVSSGMTDETNSLTINN-----NSDDLRLR- 307

RESULT 6  
US-08-961-083-118  
; Sequence 118, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961, 083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36, 373  
 REFERENCE/DOCKET NUMBER: PB340P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 118:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1040 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-961-083-118

Query Match 3.4%; Score 144; DB 4; Length 1040;  
 Best Local Similarity 19.2%; Pred. No. 0.024;  
 Matches 154; Conservative 111; Mismatches 284; Indels 252; Gaps 38;

QY 127 IKVDGKYYV-YLKDAAHADNVRTKEEINRQKQEHQSOREGGTPRND-----G 172  
 Db 76 LKIEGYQQYIGYIK-TKKQDNTELSRVTGKYSAQRDSQPNSTKTSDVVHSADLEWNQGQG 134

QY 173 AVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYPKNELSASELAAEAFL 232  
 Db 135 KVSL--QGEASGDDG-----LSEKSSIAADNLSSNDSFA 166

QY 233 SGRRGNLNSRSRTYRRQNSDNTSRTNWPSVSNPGTTNTTSNNNSNTNSQASQNSNDISLK 292  
 Db 167 S-----QVEONPDHKGESVVRPTVPEQGNPVSATIVOSAEEEVLATND----R 211

QY 293 OLYKLPLSQRHVESDG-----LVF-----DPAQITS 318  
 Db 212 PEYKLPLETKGTQOBPGHEGEAVREDLPVYTKPLETKGTQOGPGHEGEAVREEPAYTEP 271

QY 319 RTARGVAVPHGDHYHFIPYSQMSMSELEERIARIIPLRYRSNHWVPPDSRPEQSPQOPTPEPS 378  
 Db 272 LATKGTOQEPGHE-----GKATVREETLEYTEPVATKGT---OEPEHEGERXVEEL 319

QY 379 PGPQPA-----PNL-----KIDSNSSLVSQLVR---KVGEGYVFE 411  
 Db 320 PALEVTRNRTEIQNIPYTTETEIQDPTLKNRRKIERQGQAGTRTIQEDYIVNGNVET 379

QY 412 KGISRIVYFAKDLPSETVKLNESKLSKQESVSHTLTAKKENVAPRQDEFYDCKAYNLL--TE 469  
 Db 380 KEVSRTEDA--PNEVVKVGTLVKVKPTVEITNLTKVEN---KKSITVSYNLIDTS 431

QY 470 AHKALLENKGRNSDFQALDKLLERLNDESTNKEVLVDDLAFLAPI---TH-PERLGKPN 525  
 Db 432 AVVS----AKTQVFHG-DKLVKEVDIENPAKEQVISG-LDVYTPTVTKHLTYNLGENN 484

QY 526 SQIEYTEDEVRIAQLADKYYTSDGYIFDEHHIISDEGGDAYVTPHMGHSHWIGKDSLSDKE 585  
 Db 485 E--ENTETSTQDFQI--EYKKEIKDIDSVELYGKENDR-----RRYL---SLSEAP 530

QY 586 KVAAQAYTKEKGILPPSPDADVKANPTGDSAATIYNRUVGEKRIPLVRLPYMEHT--- 641  
 Db 531 TDTAKYFVVKV-----SDRFKEMYLFPVKS-----TENTIDGY 563

QY 642 -VEVKNGNLIPHKOHYHNIKEAWFDDHTY-----KAPNGYT-LEDLFATIK----Y 687  
 Db 564 KVTVAVDQOLVEEGTGYK-----DDXTFTVAKSKAEQPGVUTSFKQLVTAMQSNLGSV 616

QY 688 YVEHPDERPHSNDGWNASEHVLGKKDHS-----EDPNKNFKADE--EPVEET 733  
 Db 617 YTLASDM-----TADEVSLGDKQTSYLTGAFTGSLIGSDGCKSYAIYDLSKPLFDT 667

QY 734 PAAPEPVPOVETEKVEAQOLKEAEVLLAKVTDSSL-----KANATELAGLRNNLTLQI 785  
 Db 668 LNGATVRDLDIKTVSADSKENVAALAKAANSANTINV 727

Query Match 3.3%; Score 140; DB 4; Length 1503;  
 Best Local Similarity 19.4%; Pred. No. 0.085;  
 Matches 150; Conservative 119; Mismatches 275; Indels 228; Gaps 38;

QY 54 TPDEVSREGINAEQIVIKILTQDGYVTSHGD-----HYHYHYG-KVYDAAITISEELL 104  
 Db 582 TGPELSQLTALSVELEESSTEDDFQOSSTDPKDSSLPGDLHVTSGPESPENNIF---- 636

QY 105 MKDPNYKLKDEDIVNEVKGYYVIKVGKYYVYLDAAHADNVRTKEEINRQKQEHQSORE 164  
 Db 637 ---NDVDKSEDLPSPHQKIFDLMELNG-VQADFKPATLSSLD----NPKESVITGHFE 686

QY 165 GGTPRNDGAVALARSQGRYTTDDGYIFNASDI-IEDTGDAYIVPHGDHYHYPKNELSAS 223  
 Db 687 KEKPRK-----IFDSEPLCLSDLN----LMHQDNF----DPLNVO 717

QY 224 ELAAEAFLSGRGNLNSRSRTYRRQNSDNTSRTNWPSVSNEGTT----INTNSNNNTNS 279  
 Db 718 ELSENFLFLQEKNLKGSLSKSEHINDLOT----ELKNAGFTEAMLETSCRNSLDTEL 771

QY 280 QASQSNIDSLLKQLYKLPLSQRHVESDG-----LVFDAQITSRTARGVAVPHGDHYH 333  
 | ::| ||| | :| :| | :| | :| | :| :| :| :| :|  
 Db 772 QFAENKPGLSSL-----QENVSTKGDDTDVMLGDTLSTSLOSSPEWQVP----- 816  
 ; MOLECULE TYPE: protein  
 QY 334 FIPYSOMSELEERIARIPILRVSRNHWWPDSRPEQQSPQPT-----PEP-----SPGP 381  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 817 --PTS--FETEETPRRV-----PPDSLPTQGETQOPTCLDVIVPEDCLHQDISPA 862  
 ;  
 QY 382 QPAPNLKIDSNSLVSOLVRKVGEYVFEEKGISRYFAKDLPLPSETVKNLESKLSKQESV 441  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 863 VTVP-VEILSTDARTHSLDNR-----SQDSPGESEFTL--RLTESDSV 902  
 ;  
 QY 442 -SHTLTAKKENVAPR---DQEFYDKAYNLTEAHKALFENKGGRNSDFQALDK----- 489  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 903 LADDILASRVSVGSSLPELQGQELHNKPFSEDHHSHRRLEKNLEAVETLNQNSKDAKEA 962  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 QY 490 -LLERLNDESTNKEVLVDDLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSD 548  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 963 GLVSAVLSSDSTSODSLLEDLSAPFPASEPS-LETPS-LESV----- 1003  
 ;  
 QY 549 GYIFDEHDIISDEGGDAYVTPHMGHSHHWIGKDSLSDKEKVAQAQYTKE----KGILPPSP 603  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1004 ----DVHEALLDLSLGSHTP-----QKLVLPDKPADSGYETENLESPEWTLHPAP 1048  
 ;  
 QY 604 DADVKANP--TGDSAAIYNRVKGEKRIPLVRLPYMVEHTVEVKGNLIIPIHKDHYNK 661  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1049 EGTADSEPATGDDGHS----GLPPNPV-----VISDAGDGHGTEVT----- 1089  
 ;  
 QY 652 FAWFDHDTYKAPNGTYLEDLFATIKYYVEHPPDERPHSNDGWGNASEHVLGKKDHSEDPNK 721  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1090 -----ETFGTAGSQSYRD---SAYFSDNDSEPEKR-----SEEVPG-----TSPSA 1127  
 ;  
 QY 722 NFKADEEPVEETPAEPEVPOVETEKVAQLKEAE--VLLAKVTDSSLKANAT 771  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1128 LVLVQEOPLPPEPVNLPEQSOPQSCLEARSKSOPDESCLSALHNSSDEL RAT 1179  
 ;  
 RESULT 8  
 US-07-920-281C-2  
 ; Sequence 2, Application US/07920281C  
 ; Patent No. 5739026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Garoff, Henrik  
 ; APPLICANT: Liljestrom, Peter  
 ; TITLE OF INVENTION: DNA Expression Systems Based on  
 ; TITLE OF INVENTION: Alphaviruses  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 ; STREET: P.O. Box 747  
 ; CITY: Falls Church  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22040-0747  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US-07/920, 281C  
 ; FILING DATE: 13-AUG-1992  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Murphy Jr., Gerald M.  
 ; REGISTRATION NUMBER: 28, 977  
 ; REFERENCE/DOCKET NUMBER: 828-103P  
 ; TELEPHONE: 703-241-1300  
 ; TELEX: 248345  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 2431 amino acids  
 ;  
 TYPE: amino acid  
 ;  
 TOPOLOGY: linear  
 ;  
 MOLECULE TYPE: protein  
 ;  
 US-07-920-281C-2  
 ;  
 Query Match 3.3%; Score 140; DB 1; Length 2431;  
 Best Local Similarity 19.7%; Pred. No. 0.18; Mismatches 253; Indels 212; Gaps 34;  
 Matches 137; Conservative 93; InDelS 212; Gaps 34;  
 ;  
 QY 76 QGYVTSHGDHYHYNG-KVYDYAI TSEELLMDPNYKLKDDEDIVNEVKGGYVIKVDGKY 134  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1523 KGYSTTDGSLSYFEGTKFNQAAIDMAEILTLMWPRLOEANEQICLYALGETM----- 1574  
 ;  
 QY 135 VYKDAAHADNYRTKEEINRQKOEHSQHREGGTPRNDGAVALARSQGRYTDDGYIFENAS 194  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1575 -----DNIRSKCPVN-----DSPSSTPPRT-VPCICR-----YAMTAE 1606  
 ;  
 QY 195 DILEDTG-----DAYIVPHGDHYHYIPKNELSASELAAAEEAFISGRGNLNSRTYR 245  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1607 RIARLRSHQVKSMMVWCSFFLP-----KYHVDGVQVKVCKVLLFDPTV-----SVVSPRKYA 1660  
 ;  
 QY 246 RQNSDNTSRT-----NWVPSVSNPGBTNTNTSNNNTNSQASQNSNDISLLKQLYKLPL 299  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1661 ASTTDHSDRSLRGFDLW-----TDSSTASDTMSLPSLQSCDIDSIVEMAPIV 1712  
 ;  
 QY 300 -SQRHVESDGLVFDPAQTSRTARGVAVPHGDHYHFIPYSQMSELEERIARIPIHYRSN 358  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1713 TADVHPEPAGIADLAADVHPEA-----DHV-----DLENPIP---PPPKRA 1752  
 ;  
 QY 359 HWVPPDSRPEQSPQPTPEPSPGPOAPNLKI-----DSNSSLVSQLVRKVGEYVFEEKG 413  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1753 AYLASRAAERPVPAPR-KPTPAPRTAFRNKLPLTFGFDFDEHEVDALASGITFGDFDDVLR 1811  
 ;  
 QY 414 ISR---YVFAKDLPLSETVKNLESKLSKQESWSHTLAKKENVAPRQEFYDKAYNLTEA 470  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1812 LGRAGAYTFFSDTGS---GHLOOKSVRQ---HNLOCAQDVAQEEKMWPK---LDTER 1861  
 ;  
 QY 471 HKALF-----ENKGGRNSDFQALDKLLERLNDESTNKEVLVDDLAFLAP---ITHP 518  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1862 EKLLLKMQMHPSEANKSRYQS-RKVENMKATVDRLLTSGARLYTGADVGRIFTYAVRP 1920  
 ;  
 QY 519 ERLGKPNNSOIEYTEDEVRIA---QLADKYTTSDGY-IDEHDHDIISDEGGDAYVTPHMGHS 573  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1921 RPVYSPTVIERFSSPDVAIAACNEYLRSNYPVTASYQTIDEYDAYLDMV----- 1970  
 ;  
 QY 574 HWIGKDSLSDKE---KVAQAQYTKERGI-----LPPSP-----DADVKAN----- 610  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1971 ---GSDSCLDRATFCPAKLRCYPKHAYHQPTVRSAVPSPFQNTLQNVLAAATKRNCNT 2027  
 ;  
 QY 611 -----PTGDSAAIYN-----RVKGEKR----- 628  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2028 QMRELPTMDS-AVFNVECFKRYACSGEYWEYAKOPIRITTENITYVTKLKGPKAAAL 2085  
 ;  
 QY 629 -----IPLVRLPYMVEHTVEVKGNLIIPIHKDH 656  
 | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2086 FAKTHNLVPLQEVP-MDRFTVDMKRDVKVTPGTH 2119  
 ;  
 RESULT 9  
 US-08-466-277-2  
 ; Sequence 2, Application US/08466277  
 ; Patent No. 6190666  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Garoff, Henrik  
 ; APPLICANT: Liljestrom, Peter  
 ; TITLE OF INVENTION: DNA Expression Systems Based on  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 ; STREET: P.O. Box 747

CITY: Falls Church  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,277  
 FILING DATE: 06-Jun-1995  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/920,281  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Murphy Jr., Gerald M.  
 REFERENCE/DOCKET NUMBER: 28,977

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-241-1300  
 TELEFAX: 703-241-2848  
 TELEX: 248345

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 2431 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-08-466-277-2

Query Match  
 Best Local Similarity 3.3%; Score 140; DB 4; Length 2431;  
 Matches 137; Conservative 93; Mismatches 253; Indels 212; Gaps 34;

QY 76 QGYVVTSHGDHYHYNG-KVPYDAIISSEELMKDPNPKLKDDEIVNEVKGGYVIKUDGKVY 134  
 Db 1523 KGYSTTDGSILSYFEGTKFNQAAIDMAEILTLWPRLQEANEQICLYALGETM----- 1574

QY 135 VYLKDAAHADNRTRKEEINRQKQEHQSQHREGGTPRNDGAVALARRSGRTYDDGYIFNAS 194  
 Db 1575 -----DNIRSKCPVN-----DSDSSTPPRT-VPLCLR-----YAMTAE 1606

QY 195 DIEDTG-----DAYIVPHGDHYHYIPKNELSASELAAAEEAFLSGRGNLNSNSRTYR 245  
 Db 1607 RIARLRSHQVKSMVVYCSSFPLP---KYHVIGVQVKCEKVLFDPTV--SVVSPRKYA 1660

QY 246 RQNSDNTSRT-----NWVPSVSNPGBTNTNTSNNNTNSQASQNSNDISLLKOLYKLPL 299  
 Db 1661 ASTTDHSRSLRGFDLDW-----TDSSTSASDTMSLPSLQLQSCDIDSIVEPMAPIW 1712

QY 300 -SQRHVESDGLVFDPQITSRTARGVAWPHGDHYHFIPIYSOMSELLEERIARIPLYRSN 358  
 Db 1713 TADVHPEPAGIADLAADVHPEPA-----DHV-----DLENPIP---PPRPKRA 1752

QY 359 HWVPDSRPEQSPQPTPEPSPGPQPOPAPNLKI-----DSNSSLVSQLVRKGEGYVFEKG 413  
 Db 1753 AYLASRAERPVPAWR-KPTPAAPTAFRNKLPLITFGDFDEHEVDALASGITFGDFDDVLR 1811

QY 414 ISR---YVFAKDLPSSETVKLESKLSKOESVSHTLTAKKENVAPRDQEFYDKAYNLTEA 470  
 Db 1812 LGRAGAYIFSSDTGS---GHLOQKSVRQ---HNLOCAOLDAVQEEKMWPPK---LDTER 1861

QY 471 HKALF-----ENKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHP 518  
 Db 1862 EKLILLKMQMPSEANKSRYQS-RKVENMKATVWDRLTS GARLYTGADVGRIPYAVRYP 1920

QY 519 ERLGKPNSQLEYTEDEVRIA---QLADKTTSDGY-TFDEHDILSDEGGDAYVTPHMGHS 573  
 Db 1921 RPVYSPVIERFSSPDVAIAACNEYLSRNYPTVASYQITDEYDAYLDMVD----- 1970

---

RESULT 10  
 US-08-257-073-5  
 Sequence 5, Application US/08257073  
 Patent No. 5766597

GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo  
 APPLICANT: de Taisne, Charles  
 TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE  
 NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtis, Morris & Safford, P.C.  
 STREET: 530 Fifth Avenue, 25th Floor  
 CITY: New York  
 STATE: New York  
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 09-JUN-1994  
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,783  
 FILING DATE: 11-JUN-1993  
 PRIOR APPLICATION DATA:  
 FILING DATE: 20-MAR-1991  
 APPLICATION NUMBER: US 07/852,305  
 FILING DATE: 18-MAR-1992  
 PRIOR APPLICATION DATA:  
 FILING DATE: 09-JUN-1991  
 APPLICATION NUMBER: US 07/672,183  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REFERENCE/DOCKET NUMBER: 25,506  
 REGISTRATION NUMBER: 454310-2570

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 TELEX: 425066 CURTMS

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 740 amino acids

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal

US-08-257-073-5

---

Query Match  
 Best Local Similarity 3.2%; Score 135.5; DB 1; Length 740;  
 Matches 145; Conservative 109; Mismatches 262; Indels 305; Gaps 35;

QY 4 NKKYLV--GSAALILSVCYELGLYQARTVKENNRSVYIDGKQATQKTENLTPDEVSK 60



Db 515 GYTKKENGL--WVNTKEPIETTSISGEKVWDDKDNQDGKRPEKVSVNLLANGEVKVTLID 572  
 Qy 457 -----QEF----YDKAYNL---LTEAH-----KALFENK----- 478  
 ; | |  
 ; || : ; : | |  
 Db 573 VTSETNWRYEKFDLPKYDEGKKIETYVTEDHVKDYTIDINGTTITNKVTPGETSATVTKN 632  
 ; | |  
 ; | |  
 Qy 479 ---GRNSDFOALDKLRL--NDESTNKEKLVDLLAFLAPITHPERLGKPNSQIEYTED 533  
 ; | |  
 ; | |  
 Db 633 WDDNNNQDGKRPTEKVELYQDGKATGKTAILNESNNWHTWTGGLDEKAK-GQQVKYTV 691  
 ; | |  
 ; | |  
 Qy 534 EVRIAQOLADKYYTSDGYT-FDEHD---LISDEGDAYTPHMGHSHWIGDS----- 580  
 ; | |  
 ; | |  
 Db 692 EL-----TKVKGYTHVVDNNNDMGNLIVTNKYTPETTSISGEKVWDDKDNQDGKRPE 742  
 ; | |  
 ; | |  
 Qy 581 -----LSDKEKVAQAQAYTKEKGILPPSPDADVKAANPTGDSAAIYNRKGEKRIPLVRL 634  
 ; | |  
 ; | |  
 Db 743 KVSVNLLADGEKVKTLDVSE-----TNKYEFKDLPKYD-----EGKKIEYTVTE 788  
 ; | |  
 ; | |  
 Qy 635 PYMVEHTVEVKNGNLI-----IPHKDHVHN-----IKFAWFDD----- 667  
 ; | |  
 ; | |  
 Db 789 DHVKDYTTDI-NGTTITNKYTPGETSATVTKNWDNNNQDGKRPTEKVELYQDGKATGK 847  
 ; | |  
 ; | |  
 Qy 668 -----HTY----KAPN--GYTLEDFATIKYVVEHDERPHSNDGWGN---- 704  
 ; | |  
 ; | |  
 Db 848 TAILNESNNWHTWGLDEKAKGQOVKTYVEEL-TKVKGYTHV-----NNDMGNLIWT 901  
 ; | |  
 ; | |  
 Qy 705 -----ASEHWLGKKDHSED--PNK--NFKADEEPVEETPPE-----VP 740  
 ; | |  
 ; | |  
 Db 902 NKYTPETTSISGEKVWDDKDNQDGKRPEKVSVNLLANGEVKVTLDVSETVTKNWD----DNNN 1012  
 ; | |  
 ; | |  
 Qy 741 QV-ETEKVEAQOLKEAEVLLAKVTDSSLKANAT-----ETLAGLRNNLTQIMDNNS 790  
 ; | |  
 ; | |  
 Db 962 KYDEGKKIEYTVTEDH-----VKDYTTDINGTTITNKYTPGETSATVTKNWD----DNNN 1012  
 ; | |  
 ; | |  
 Qy 791 IMAEAKLLALLGSNPSSVSKE 813  
 ; | |  
 ; | |  
 Db 1013 -----QDGKRPTEKVE 1024  
 ; | |  
 ; | |  
 RESULT 12  
 US-08-015-973-1  
 Sequence 1, Application US/08015973  
 ; Patent No. 5604094  
 GENERAL INFORMATION:  
 APPLICANT: Schlessinger, Joseph  
 TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/015,973  
 FILING DATE: 10-FEB-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Misrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 7683-021  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)790-9090  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
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 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
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 ; MOLECULE TYPE: protein  
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 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
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 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
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Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Topology: linear  
 ; MOLECULE TYPE: protein  
 US-08-015-973-1

Query Match 3.2%; Score 135; DB 1; Length 2308;  
 Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
 Matches 169; Conservative 123; Top

RESULT 13  
US-08-448-164-1  
; Sequence 1, Application US/08448164  
; Patent No. 5925536  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHATASE-BETA  
; TITLE OF INVENTION: PHOSPHATASE-BETA  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,164  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/015,973  
; FILING DATE: 10-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7683-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)790-9090  
; TELEFAX: (212)869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2308 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-448-164-1

Query Match 3.2%; Score 135; DB 2; Length 2308;  
Best Local Similarity 19.2%; Pred. No. 0.4;  
Matches 169; Conservative 123; Mismatches 276; Indels 310; Gaps 44;

QY 71 RKITDQGYVTSHGDHYHYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKD 130  
Db 954 VGVTVQGSLSFGPSHI-----PIPKSSLITPTASLQLPHTALSG-----D 993  
QY 131 GKYYVYLKDAAHADNVRTKEEINRQKQEHQSQHREGGTPRNDAVAL-----ARSQGRYT 184  
Db 994 GEW-----SGASSDS-----EFLLPDTDGLTALNISSPVVAEFTY 1030  
QY 185 T----DDGYIFNAASDITEDTGDAYIVPHGDHYH----IPK----NELSAELAAE 229  
Db 1031 TSVFGDDNKALKSKSEIYGNETELQIPPSFNEMVYPSESTVMPNMYDNVNKLNASQETSV 1090  
QY 230 AFLSGRG-----NLSNSRTYR-RQNSDNTS----RTNWVP 259  
Db 1091 SISSTKGMFPGLSLAHTTTKVFHDHETSQVPENNFSVQOPTHTVSQASGDTSLKPVLSANSEP 1150  
QY 260 SVSNPGTT-----NTNTSNNNTNSQAS-QSNDIDSLLKQLYKLPLSQRHVES 306  
Db 1151 ASSDPASSEMLSPSTQLLFYETSASFTEVLLQPSFOASDVTLLKTV--LPA---VPS 1204  
QY 307 DGLVFDPAQ-----ITSRTARGVAVPHGDHYHFTPYSQMSELEERIARIIPLRY 355  
Db 1205 DPLILVETPKVKDISSTMHLIVSNSASSENMLHSTSVPVFDVSPTSHMHSAISLQGLTISY 1264

RESULT 14  
US-08-081-929-2  
; Sequence 2, Application US/08081929  
; Patent No. 6160090  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Barnea, Gilad  
; APPLICANT: Grumet, Martin H.  
; APPLICANT: Margolis, Richard U.  
; TITLE OF INVENTION: A NEW CLASS OF RTPPasses: THEIR  
; TITLE OF INVENTION: STRUCTURAL DOMAINS AND LIGANDS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,929  
; FILING DATE: 23-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30742  
; REFERENCE/DOCKET NUMBER: 7683-041-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2308 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: unknown

US-08-081-929-2

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Query Match 3.2%; Score 135; DB 4; Length 2308;  
Best Local Similarity 19.2%; Pred. No. 0.4; Mismatches 276; Indels 310; Gaps 44;  
Matches 169; Conservative 123; Mismatches 276; Indels 310; Gaps 44;

Qy 71 IKITDQGYVTSHGDHYHYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKD 130  
Db 954 VGVTYQGSLFSGPSHI----PIPKSSLITPTASLQLQPTHALSG----D 993

Qy 131 GKYYVYVLKDAAHADNVRTEKEINRQKQEHQSQRREGTPRNDGAVAL----ARSQGRYT 184  
Db 994 GEW----SGASSDS-----EFLPDTDGLTALNISSPPVVAEFTYT 1030

Qy 185 T----DDGYIFNASDIDIETDGTDAYIVPHGDHYH----IPK----NELSASELAAAE 229  
Db 1031 TSVFGDDNKALKSKSEIYGNETELOQIPSPFNEMVYPSESTVMPNMVDNVNLKLNASQESTV 1090

Qy 230 AFLSGRG-----NLSNSRTYR-RQNSNTS----RTNWVP 259  
Db 1091 SISSTKGMFPGLSAHTTTKVFDEHEISQVPPENNFSVQOPTHTVSQASGDTSLKPVLSANSEP 1150

Qy 260 SVSNPCTT-----NTNTSNNNSNTNSQAS-QSNDIDSLLKOLYKPLSORHVES 306  
Db 1151 ASSDPASSEMMLSPSTQOLLFYETTSASFSTEVLLQPSFQASDVDTLLKTW--LPA---VPS 1204

Qy 307 DGLWFDAQ-----ITSRTARGAVAVPHGDHYHFIPIYSQMSELEERRARIPIRLY 355  
Db 1205 DPILVETPKVDKISSSTMLHLIVSNSASSENMLHSTSVPVFDVSPSHMHSASLQGLITISY 1264

Qy 356 RSNHWVPPDSRPEQQSPQPTPEPPSPGPQPOPAPNLKIDSNSSLVLSQLYRKVGEGYWFEERGIS 415  
Db 1265 ASEKYEPVPLLKSESSHQVVP-----SLYSNDELFOQTANLEINQAH--PPKG-- 1308

Qy 416 RYVFAKKLPS--ETVKNLESKLSKQESVSHILTAKKENVAPR-----DOFYDKAY 464  
Db 1309 RHFATPVLSIDEPLNTLINKLHSDEI--LTSTKSSVTGKVFAGIPTVASDTFVSTDH 1365

Qy 465 NL-LTEAH-----KALFENKG-----479  
Db 1366 SVPIGNGHVALTAVSPHRGSVTSTKLFLPSKATSELHSAKSDAGLVGGGEDGTTDDG 1425

Qy 480 -----RNSDFQALDKLLERNDESTNKEKLVDDLLAFLAPITHPERLGKPNQIEY-- 530  
Db 1426 DDDDDDRGSDGLSIHKCMS-CSSYRESQEKMND----SDTHENSLMDQNPISYLS 1478

Qy 531 --TEDEVRIAQLADKYTT-----SDGYIFDEDEHD-----ISDE 561  
Db 1479 ENSEEDNRVTSSDSQTMGRSPGKSPSANGLSQKHNDGK--EENDIQGALLPLSPE 1536

Qy 562 GDAYVTPHMGHSHWIGK--DSLSDKEKVA-AQAYTKEK--GIL-----PPS 602  
Db 1537 SKAWAVLTSDEESEGGQGQTSDSLNLNETSTDFSEADTNEKDADGILAAGDSEITPGFPQOS 1596

Qy 603 PDAADV-----KANPTGDSAIIYNRVKGEKR--IPLVRLPYMVEHTVEVKN 646  
Db 1597 PTSSVTSENSEVFHSEAEASNSSHESRIGLAEGLSEKKAVIPLVIVSALTIFICLWVL 1656

Qy 647 GNLIIPHK--DHYHNIKEAWFDDHTY----KAPNGYTLLEDLFA-TIKYVVEHPDE 694  
Db 1657 GILIYWRKCFQTAHF-----YLEDSTSPPRVISTPPTRIFPIFISDDVGAIPIKHFKHVAD 1710

Qy 695 RPHSNDGWGNASEHV----LG----KKDHSEDPNKN 722  
Db 1711 L-HASSGTFEEFEEVOSCTVLDGITADSSNHPDNKHN 1747

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RESULT 15  
5268270-2  
;Patent No. 5268270  
;APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johannes  
;TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM  
;SEQ ID NO:2:  
;LENGTH: 1507  
;5268270-2

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/171,872  
FILING DATE: 01-JUL-1987  
NUMBER OF SEQUENCES: 6

Query Match 3.1%; Score 133.5; DB 6; Length 1507;  
Best Local Similarity 18.1%; Pred. No. 0.26; Mismatches 305; Indels 399; Gaps 53;  
Matches 183; Conservative 125; Mismatches 305; Indels 399; Gaps 53;

Qy 73 ITDQGYVTSHG-----DHYHYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGG 124  
Db 523 ITNPNSLSVHSIIONDYDDEDDSYVYPRRPIPQ--GKDLYYYKNRY-----  
Qy 125 YVKVUDGKYVYVLKDAAHADN----VRTKELIENRQKQEHQSQR----EGG----TP 168  
Db 567 YALKSGGRNLPMPENGVAENNDWIFMGYTOEEARKNAMNHKNRRRTGDEGGFDEENGK 626

Qy 169 RNDGAVAL----ARSQGRYTDDGYIFNASDIDIETDGTDAYI----VPHGDHY----NLSNSRTYR 245  
Db 627 GHNGALNLNFNGKSAQNRELLTGGANLNGK- ISVTQGNVNLLSGRPTPHARDEVNKKSKARK 685

Qy 213 --HYIPKNEL-----SASELAA--AEFLSGRG-----NLSNSRTYR 245  
Db 686 DAHFSKNNEVVFEDDWINRTEKAELIAVNQASAFSSGRNWDDITANITATDNAVKNLGYK 745

Qy 246 RQNSNTS-RTNWVPSVS-NPGTIN-----TNTSNNNSNTNSQAS-----282  
Db 746 --NGDEVCVRSRDYTGVTCTNTGNLSDKALNSFDXATKINGNVNLNQNAALVLGKAALWGK 803

Qy 283 --QSNDIDSLLK-----QIYKLPLSQRH-----304  
Db 804 IQGQGNSRVSLSNQHSKWHLTGDSQVHNLSLADSHIHLNNASDAQSANKYHTIKINHLSGN 863

Qy 305 -----ESDGL-VFDDPAQITSRTARGVA 325  
Db 864 GHFHYLTDLAKNLGDKVLVKEASAGHYQLHQNKGTGEPNQEGLDFDASSVQDRSRLFV 923

Qy 326 VPHGDHYHFTPIYSQMS--ELEERIARIPLRYRSNHWWVPSRPEQQSPQPT-----374  
Db 924 LAN----HYVLGALRTIKTENGITRLY-----NPYAGNGRPVKAQEQVKRQQAEEKVARDQEEAK 973

Qy 375 -----PE-----PSPGPQAPNLKIDSNSL-----SOLV 400  
Db 974 KATQTDGAQIAKPNQVAPPSPQANQAEELRQOAKAEQVKRQQAEEKVARDQEEAK 1033

Qy 401 RKVGE-GYVFEERGISRYVEAKDLPSSETVKLKSQKQESVSHLTAK-----KENVAP 454  
Db 1034 RKAETIARQQEEARAKAELAKOKAEEKAERKARELARQAEASHQANAKPKRRRRAILP 1093

Qy 455 RD-----  
Db 1094 RPPAPVFSLLDYDAKDNSESSIGNALRVPIRMGRRELINDYEEPLEEDEEEERRQAT 1153

Qy 472 KALFENGRNSDFQALDKLLERNDESTNKEKLVDDLLAFLAPITHPERLGKPNQIEY 531  
Db 1154 Q--FHKSRSNR--RAISS--EPSSDEDASESVSTD-----KHPQDNTELHEKVET 1199

Qy 532 EDEVRIAQ-----LADKYTTSDGYIFDE----HDLISDEGDAVTPHMGHSHWIGK 579  
Db 1200 GLQPRAAQPRTQAAAQADAVSTNTNSALSDAMASTQSILLDTG-AYLTRH-----IAQK 1252

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QY	580	SLSDKEKVAQAYTKEKGILPPSPDADVKANPTG - - - DSAAAIYNRVKGEEKRIPVLRLPY	636
Db	1253	SRADAEEK - - - - - NSVWMENTGYGRDYASAQYRRFSSKRQTQIGIDR	1294

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Job time: 160 sec